us-10-082-830-98.rge

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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i.e.: US-10-082-830-98 ifect score: B63 uring table: I atgggtttggtcattca I atgggtttggtcattca I atgggtttggtcattca at number of hits satisfying cho immum DB seq length: Oithur and	OM nucleic - nucleic search, using sw model	
### Biggitting trace of the service	on: August 14, 2004, 07:10:17; Search t (without 9989.844	Seconds updates/
### 10507177 NUC 3470272 seqs, 21671516995 residues	US-10-082-830-98 score: 863 : 1 atgggtttggtcattcaact	86
1: 3470272 segs, 21671516995 residues Imber of hits satisfying chosen parameters: 694054 DB seq length: 0 DB seq length: 0 DB seq length: 0 Maximum Match 100* Listing first 45 summaries GenEmbl:* 1: gb_ba:* 2: gb_htg:* 4: gb_on:* 5: gb_on:* 1: gb_bi:* 6: gb_pat:* 7: gb_pi:* 11: gb_re:* 11: gb_re:* 12: gb_re:* 13: gb_ni:* 14: gb_vi:* 15: gb_re:* 16: em_fun:* 17: em_hum:* 18: em_pi:* 21: em_or:* 22: em_or:* 23: em_or:* 24: em_pi:* 25: em_or:* 25: em_or:* 26: em_tg_other:* 27: em_tg_other:* 28: em_htg_other:* 29: em_htg_other:* 21: em_htg_other:* 23: em_htg_other:* 24: em_htg_other:* 25: em_htg_other:* 26: em_htg_other:* 27: em_htg_other:* 28: em_htg_other:* 29: em_htg_other:* 21: em_htg_other:* 23: em_htg_other:* 24: em_htg_other:* 25: em_htg_other:* 26: em_htg_other:* 27: em_htg_other:* 28: em_htg_other:* 28: em_htg_other:* 29: em_htg_other:* 20: em_htg_other:* 2	coring table: IDENTITY NUC Gapop 10.0 , Gapext	
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41: em_incgo_other: Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Direct Submission

Spirer, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Backerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Bacra, N., Beckerly, R., Collins, S., Collymore, A., Cooke, P., Cokerellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Howland, J., Johnson, R., Jonsson, R., Jonsson, R., McZere, K., McZere, R., McZere, McZere, R., McZere, R
                                                                               38713 GTTTGCAAATATGTTGCCTAGCTTGTGGCTTGACTTTTCAGTTTCTTCAGTATTACATTT 88654
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Homo sapiens clone RP11-3B17, WORKING DRAFT SEQUENCE, 14 unordered
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                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Mammalia, Butheria, Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 176269)
Birran,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-3B17
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
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Center clone name: 3 B 17
Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.shgc.stanford.edu
www.shgc.stanford.edu
www.shgc.stanford.edu
Woulity: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 165.6kb). It is clipped at the overlap with AC093292.
The number of bases overlapped is 53223.
Location/Qualifiers
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Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases I to 162100)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                             Submitted (27-MAR. 2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 27, 2002 this sequence version replaced gi:19224833. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center
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2 (bases 1 to 162100)
DOE Joint Genome Institute.
Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, 16-AUG-2001) Production Sequencing Facility, 16-AUG-2000 Mitchell Drive, Walnut Creek, CA 3 (bases 1 to 162100)
DOE Joint Genome Institute.
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Pred. No. 9.2e-97;
0; Mismatches 231; Indels
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-53019"
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Matches 625; Conservative (
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                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 168178 bases at least Q40
Consensus quality: 172094 bases at least Q30
Consensus quality: 173529 bases at least Q20
Insert size: 150000; agarose-fp
Insert size: 17469; sum-of-contigs
Quality coverage: 6.0 in Q20 bases; sum-of-contigs
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1316 1415; gap of 100 bp
2587: contig of 1172 bp in length
2588 2947: contig of 100 bp
2688 2947: contig of 100 bp
4582: contig of 100 bp
4582: contig of 100 bp
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4682: gap of 100 bp
4683: gap of 100 bp
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6704: gap of 100 bp
6704: contig of 5295 bp in length
6705: contig of 5295 bp in length
6706: gap of 100 bp
6707: contig of 5295 bp in length
6708: gap of 100 bp
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99133 TGGTTTGATGATTTTTTACATTATATAGTATTACATTCCATGGATAGTTCTCAGTAGATAA 99074
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72.8%;
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90445: gap of 100 bp

104918: contig of 14873 bp in length

105018: gap of 100 bp

109986: gap of 100 bp

120755: contig of 10769 bp in length

120755: gap of 100 bp

133558: contig of 10769 bp in length

120855: gap of 100 bp

134058: gap of 100 bp

141783: contig of 725 bp in length

141883: gap of 100 bp

147865: contig of 592 bp in length

147865: contig of 592 bp in length

147865: gap of 100 bp

154337: contig of 6872 bp in length
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                                                                                                                                                                                                                                                                         AL845425 15-NOV-2002 DAN linear HTG 15-NOV-2002 Danio rerio clone CH211-123B21, WORKING DRAFT SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cyctinopterygii; Neoprerygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 154837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 149574 bases at least Q40
Consensus quality: 151215 bases at least Q40
Consensus quality: 152331 bases at least Q30
Insert size: 153037; aum-of-contigs
Quality coverage: 4.53x in Q20 bases; sum-of-contigs Quality
coverage: 4.24x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2: gap of 100 bp

5: contig of 4804 bp in length

5: gap of 100 bp

6: contig of 6079 bp in length

6: gap of 100 bp
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gap of 100 bp
contig of 5160 bp in length
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gap of 10
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HTG; HTGS PHASE1; HTGS DRAFT.
Danio rerio (zebrafish)
Danio rerio
                                                                                               98355 GTAGCTGAGCCAATGAT 98338
                                                 841 GIAGCIGAGACCAATGAT 858
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DEFINITION AL845324 ORIGIN g 8 144929 ATTITATITIACITIACITIACITITITITITITITIATITITATITIATITIAT 144870 144930 145230 145110 145050 144990 145530 145470 145350 145290 ò 619 619 739 139 199 799 140 INGCGINGCINCICATITIGACCIAITITAAACAGGCCICITIAAAIATATACACITCICIG 145529 TTTTGTTTTATTTGATCTTTTACTCTTTACTTTAATTTTATTTTATCGTTACTTT 260 TAAGATGTCAAACTGTTTTCTAAAAGTGTTTTTAACTATTATATGTCAATTTTGAA 320 CAGCTCTTTCACTTACTAGCAATTTATTATCAGCAACACTTGTTATTGTCAGACTTTTAA 145349 TÄTTTAATTTATTTTATCTTTÄCTTTTTACTTTATCTAGTTTATTTATTTATT 145169 ITTTACTTTTAATTTAATTCATTTATTTTTTTTTATTTTTACGCCACTTTTTTCTT 145049 TATTICATTIATTITIATTITIATGITIACTITITATATTITAGATTITAAATGIATIAC 680 AAATCGACATTATGATATATCTTCCAAAATTTTAATAATTTTGTCTTTTTCACATT 80 TTATATAGTATTACATTCCATGGATAGTTCTCAGTAGATAATCCTCCTATTGTTTAACAT TAGTGTATGCTAGAAATGGAGTGGCTGGAATAAAAGTGGCTGAATCATCTTCAACTCTAG 620 NNNNNNNGTGATCATATTTATGTTTTGCTCATTTAAAAAAACCTGGTTAAATATTTCAC TITAAGITTATGAGATATATCCATGITGAATTITGIAGCIGIGGITTGATGATTTTTACA Gaps , 0 1 8.4%; Score 72.2; DB 2; Length 154837; Similarity 32.3%; Pred. No. 0.0013; Conservative 0; Mismatches 546; Indels 0; fragment_chain:5" 141884. 147865 //note="assembly_fragment:00008 fragment_chain:5" 147966. 154837 /note="assembly_fragment:00289 fragment_chaln:5 clone_end:8P6 vector_side:right" Thiairtrairtrairtrair 144844 GTITITCCCTATGAAATAAATTATTT 825 Query Matt. That Local Sime. 260; C misc_feature misc_feature 740 200 800 200 144869 20 ORIGIN ò d d g δ g δ g d ö 임 8 ò à à ð g ð g ò g à 유 8 Вþ $\overset{\sim}{\circ}$ g

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· 0 9177 24-SEP-2003 2 unordered 79 Direct Submission
Submitted (23-SEP-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 24, 2003 this sequence version replaced gi:31616709. AL845324.15 GI:35209193
HTG; HTGS_PRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cyptiniformes; Cyprinidae; Danio.
1 (bases 1 to 161204) 9118 irriratritatructariricaarrerruccirirraarriraarriratarraraa TIATATAGTATTACATTCCATGGATAGTTCTCAGTAGATAATCCTCCTATTGTTTAACAT 20 TITAAGTITAIGAGATATAICCAIGIIGAATITITGIAGCIGIGGITIGAIGAITITIACA Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 161092 bases at least Q40
Consensus quality: 161096 bases at least Q40
Consensus quality: 161100 bases at least Q20
Insert size: 161104; sum-of-contigs
Insert size: 166733; 4.8% error; agarose-fp
Quality coverage: 14.82x in Q20 bases; sum-of-contigs Quality
coverage: 14.32x in Q20 bases; agarose-fp NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. .. 0 AL845324 161204 bp DNA linear HTG Danio rerio clone CH211-122L14, WORKING DRAFT SEQUENCE, pieces. Length 161204; 140163: contig of 140163 bp in length 140263: gap of 100 bp 161204: contig of 20941 bp in length. Query Match
8.4%; Score 72.2; DB 2;
Best Local Similarity 32.3%; Pred. No. 0.0013;
Matches 260; Conservative 0; Mismatches 546; /clone_lib="CHORI-211" 1. 146163 |note="assembly fragment:01479 fragment_chain:1" |40264. 1.041204 |note="assembly fragment:04647 fragment_chain:1" Center: Wellcome Trust Sanger Institute 1. .161204 /organism="Danio rerio" /nol_type="genomic DNA" /db_xref="taxon:7955" /clone="CH211-122114" Location/Qualifiers 140164 140264 Sehra, H misc_feature misc_feature 80 ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES ò

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC113205 183662 bp DNA linear HTG 04-MAR-2003
Mus musculus clone RP23-319G18, WORKING DRAFT SEQUENCE, 7 ordered
9598 ITTTACTTTATTTTAATTAATTCATTTATTTTTTATTTTTAATTTTACGCCACTTTTTTCTT 9657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9658 TITCITITAGATITICAGATATITITITITITITITITITITITITITITITATITIATIGIAITT 9717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGATGTCAAACTGTTTTCTAAAAGTGTTTTTAACTATTATATGTCAATTTTGAA 319
                                                                                                                                                                                                                                                                                                                                                                                                      320 CAGCTCTTTCACTTACTAGCAATTTATTATCAGCAACACTTGTTATTGTCAGACTTTTAA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       680 AAATCGACATTATGATATATTATCTTCCAAAATTTTAATAATTTTGTCTTTTTTCACATT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 NNNNNNNNGTGATCATATTTATGTTTTGCTCATTTAAAAAACCTGGTTAAATATTTCAC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       740 TTAGTCTTTAGCTCAGCTGGAATTCATTTCTGTGTGGTGTGAGATAAGTCTTTTTCAT 799
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 1836.2)
Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-319G18
                                                         TTGCGTTGCTTCTCATTTTGACCTATTTTAAACAGGCCTCTTTAAATATACACTTCTCTG
                                                                                                             9238 ritigiritairigaiciriacicririactitaritaaririraririategiaerir
                                                                                                                                                                       200 TAGTGTATGCTAGAAATGGAGTGGCTGGAATAAAAGTGGCTGAATCATCTTCAACTCTAG
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9898 TTATTTTATTTTATTTTATTT 9923
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AC113205/c
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Direct Submission

Direct Submission

Submitted (26-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases it to 18362)

Sincen, B. Nusbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Debrellano, K., Collymore, A., Cooke, P., Corum, S., Debrellano, K., Erickenia, D., Faro, S., Ferredra, D., FitzGerald, M., Gage, D., Galegan, J., Gardyna, S., Fartagerald, M., Gage, D., Galegan, J., Hagos, B., Hall, J., Horton, L., Hulme, W., Hafez, N., Hagospian, D., Hagos, B., Hall, J., Morton, L., Hulme, M., Mabbitt, R., Maclean, C., Macdonald, D., Major, J., Manning, J., Matthews, C., McCarthy, M., Mabbitt, R., Maclean, C., Micol, R., Minova, T., Macha, V., Nurphy, T., Naylor, J., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, R., Seanan, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Stubs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zaihoun, J., Sambek, L., Zimmer, A. and Zody, M. Direct, Submission
., Seaman,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 4, 2003 this sequence version replaced gi:21166295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 183062; sum-of-contigs
Quality coverage: 11.1 in Q20 bases; agarose-fp
Quality coverage: 10.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L23735
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone amen. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Ems., EMBL; Sww., SWISSEROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
56544
                                                                                                                                                                                                                                                                                                                                                                                                              AL935208 151406 bp DNA linear VRT 17-JUL-2003 Zebrafish DNA sequence from clone CH211-241N17, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-JUL-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Zish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 17, 2003 this sequence version replaced gi:32398511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyprinidae; Danio.
1 (bases 1 to 151406)
Phillimore, B.
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                                                                        TITCACATITIAGECTITAGCTCAGCTGGAATTCATTTCTGTGTGTGTGTGAGATAAG-
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CH211-241N17 is from a CHORI-211 BAC library
VECTOR: pTARBAC2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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0; Mismatches 334; Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/db xref="texon:10090"
/clone="RP23-319G18"
/clone lib="RPCI-23 Female Mouse BAC"
1.1269
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0.002;
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note="assembly_fragment"
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'note="assembly_fragment"
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'note="assembly_fragment"
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32.6%; Pred. No. 0.0033;
ive 0; Mismatches 515; Indels
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/organism="Danio rerio"
/wol type="genomic DNA"
/db_xref="texon:7955"
/clone="CH211-24.N17"
/clone_lib="CHORI-211"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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32.8%; Pred. No. 0.018;
ive 0; Mismatches 552;
                               Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with Patent: WO 0168911-A 50 20-SEP-2001;
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AX251789 6062 bp Sequence 50 from Patent W00168911. AX251789 AX251789.1 GI:15985144

synthetic construct synthetic construct

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 7 AX251789 LOCUS DEFINITION

LOCUS DEFINITION

RESULT 8 AC138074

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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S Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Chang, d., Choepel, Y., Collymore, A., Conk, A., Cook, A., Cook, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, d.S., Dodge, S., Farceira; P., FitzGrald, M., Gage, D., Galagan, J., Gardyna, S., Gords, S., Gardham, L., Hulme, M., Illev, I., Johnson, R., Hafez, N., Karteas, A., Kallas, C., Landers, T., Levine, R., Johnson, R., Lindblad-Toh, K., Liu, G., MacLean, C., Madchard, P., Madorald, P., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Mendes, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Maclon, C., Noch, D., Oliver, J., Norman, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Steperson, R., Phunkhang, P., Pierre, M., Raymond, C., Redge, Thomann, N., Steanes, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, M., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainmer, A. and Zody, M. Direct Submission
                                                      ACL38074 66993 bp DNA linear HTG 12-DEC-2002
Homo sapiens chromosome 18 clone RP13-907D8 map 18, LOW-PASS
SEGURICE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC138074.1 GI:26553381
HTG; HTGS_PHASE0.
HTG ospicens (human)
Homo sapicens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This record contains 55 individual
sequencing reads that have not been assembled into
contigor. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
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Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP13-907D8
Unpublished
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KEYWORDS
SOURCE
ORGANISM
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TITLE JOURNAL

COMMENT

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BX842689 146871 bp DNA linear HTG 03-DEC-2003 Danio rerio clone DKEY-96D22, WORKING DRAFT SEQUENCE, 11 unordered
                                                                                                                                                                                                                                     606 NNNNNNNNNNNNNNNNNNNNNNNNGTGATCATATTTATGTTTTGCTCATTTAAAAAAAACCTG 665
                                                GTTAAATATTTCACAAATCGACATTATGATATTATTATCTTCCAAAATTTTAATAATTTTG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-DEC-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                          Insert sizė: 145871; sum-of-contigs
Insert size: 162937; 4.9% error; agarose-fp
Quality coverage: 5.37x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 143802 bases at least Q40
Consensus quality: 144621 bases at least Q30
Consensus quality: 145107 bases at least Q20
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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Center: Wellcome Trust Sanger Institute
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20096: 9
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Similarity 0.0098; Pred. No. 0.0098;
No. Conservative 0; Mismatches 553; Indels 0;
contig of 1124 bp in length 3556: gap of 100 bp 3556: contig of 1100 bp in length 656: gap of 100 bp in length 782: contig of 1126 bp in length 822: gap of 100 bp 78: contig of 1126 br 78: contig of 1126 br 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig of 100 bp 78: contig o
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2 of 1126 bp in length

1 100 bp

2 0f 1199 bp in length

2 100 bp

3 of 1122 bp in length
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of 1110 bp in length
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of 1104 bp in length
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of 1084 bp in length
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/clone_lib="RPCI-13 Human Female BAC"
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of 1170 bp in
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Sequence 564 from Patent WO0200928.
AX345493
AX345493.1 GI:18493379
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Best Local Similarity 34.23
Matches 269; Conservative
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AUTHORS
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327 126341: contig of 11015 bp in length

342 12641: gap of 100 bp

440 136399: contig of 9958 bp in length

460 136499: gap of 100 bp

560 143438: contig of 6939 bp in length

439 143538: gap of 100 bp

539 146871: contig of 3333 bp in length.

Location/Qualifiers
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Pred. No. 0.01;
0; Mismatches 563; Indels
                                                                                                                            100 bp
of 31442 bp in length
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of 12660 bp in length
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of 14892 bp in length
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ragment_chain:1"
36500 .143438
note="assembly_fragment:00011"
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note="assembly_fragment:00500
ragment_chain:]"
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note="assembly_fragment:01063
ragment_chain:1"
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/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-96D22"
/clone_lib="DanioKey"
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contig
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Best Local Similarity 26.7%;
Matches 205; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 237186 bases at least Q40
Consensus quality: 237786 bases at least Q30
Consensus quality: 237961 bases at least Q20
Insert size: 238039; sum-of-contigs
Insert size: 218989; 8.9% error; agarose-fp
Quality coverage: 9.82x in Q20 bases; sum-of-contigs Quality
coverage: 11.38x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently a consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as thus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 98607: contig of 98607 bp in length

608 98707: gap of 100 bp

611 142710: contig of 43903 bp in length

611 190543: contig of 47833 bp in length

544 190643: gap of 100 bp

Location/Qualifiers
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Pred. No. 0.016;
0; Mismatches 532;
                     Center: Wellcome Trust Sanger Institute
Center code: SC
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/clone_lib="DanioKey"
1. .98607
/note="assembly_fragment:01005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98708._.142610
/note="assembly fragment:01799
fragment_chain:1"
142711...190543
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fragment_chain:1"
190644. 723939 fragment:02561
fragment_chain:1"
                                                                   --- Summary Statistics
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/db_xref="taxon:7955"
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ilarity 31.5%;
Conservative
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Best Local Similarity
Matches 245; Conserv
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                                                                                                                                                                                                                         3571 TAGTGTTTTGAGGAATCGTTATATTTTTTTAAATGGTTGTATTAATTTATATTTTTA 3630
                                                                                                                                                                                                                                                                                                                        3689 TATTIGITAAAAGITAITITAAIAGAIGAITATTITITATIGAITITAATTIGITITT 3748
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                                                                                                                                                                                                                                                                          TAAGATGTCAAACTGTTTTCTAAAAGTGTTTTTATTTTTAACTATTATGTCAATTTTTGAA 319
                                                                                                                                                                                                                                                                                                                                                                 320 CAGCTCTTTCACTTACTAGCAATTTATTATCAGCAACACTTGTTATTGTCAGACTTTTAA 379
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Submitted (24-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 15A, UK. E-mail enquiries:
Zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 24, 2003 this sequence version replaced gi:32479716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 239339)
TATATAGTATTACATT-CCATGGATAGTTCTCAGTAGATAATCCTCCTATTGTTTAACAT
                                           200 TAGIGTATGCTAGAAATGGAGTGGCTGGAATAAAAGTGGCTGAATCATCTTCAACTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3809 ITTITAAATIGAGATGITITGITITICGITITATIGAGIGITIGAATITITATATITITGG
                                                                                         TTGCGTTGCTTCTCATTTTGACCTATTTTAAACAGGCCTCTTTAAATATACACTTCTCT
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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JOURNAL
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KEYWORDS
SOURCE
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/db_xre="taxon:3702"
/db_xre="taxon:3702"
/clone="600050"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1. .1407
/note="T-DNA flanking sequence
right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAITGTTTAACATTTGCGTTGCTTCTCATTTTGACCTATTTTAAACAGGCCTCTTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          666 GITAAATAITICACAAATCGACAITAIGAIAIATIAITAICTICCAAAAITITAAIAAITITIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 NNNNNNNNNNNNNNNNNNNNNNNNGTGATCATATTATGTTTGCTCATTTAAAAAAACCTG
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genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1407;
http://dbsgap.versailles.inra.fr/publiclines/. This been generated in the framework of the French plant program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr').

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568;
                                                                                                                                    1. .1407
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/culTivar="Wassillewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65.4; DB
Pred. No. 0.062;
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Matches 263;
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PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versalles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutent line and a link to a database providing a graphical display of the insertion site are available at
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Qy 786 TAAGTCTTTTCATGTTTTTCCCTATGAATAATTATTTCCTTCTGTATT 836 Db 1140 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	LOSUS LOSUS LOCUS DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 602D05. ACCESSION AJ592058.1 GI:37941682 VERSION AJ592058.1 GI:37941682 KEYWORDS right border; T-DNA flanking sequence. SOURCE Arabidopsis thaliana (thale cress)	ORGANISM Arabidopsis thallanna Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechrold, N., Cruaud, C., DeRose, R., Pelletier, G., Lebiniec. L., Caboche, M., and Lecharn, A.,	TITLE T-DNA; integration into the Arabidopsis genome depends on sequences of pre-insertion sites JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002) MEDLINE 2236335 PUBMED 1244656 REFERENCE 2 (pases 1 to 1434) AUTHORS Balzerque, S. TITLE Direct Submission	JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Bryr cedex, FRANCE COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versalles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a	graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr). FEATURES 1. 1434 / corganism="Arabidopsis thaliana" //mol_type="genomic DNA" //cultivar="Wassillewskija" //db_xre="maxon:3702"	ouzbus" ib="Arabidopsis thaliana DNA flanking sequence rder"	Query Match Query Match Query Match Matches 267; Conservative 0; Mismatches 559; Indels 0; Gaps 0; Qy 6 TTTGGTCATTCAACTTTAAGATATATGAGATATATCATGAGATTATATATA	Db 509 INNTITITITITITITITITITITITITITITITITITI

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REFERENCE

Explains to 1453)

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Losubmitted (23-00T-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Submitted (23-00T-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Bry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at the they://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoilogen.fr). ö brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
2236355 604 125 664 126 CTATIGITIAACAITIGCGIIGCIICICAITITIGACCIAITITAAACAGGCCICITIAAA 185 724 245 784 305 ATGICAATTITGAACAGCICTITCACTTACTAGCAATTTATTATCAGCAACACTTGTTAT 365 904 964 /organism="Arabidopsis thaliana"
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/ note="T-DNA flanking sequence 186 TATACACTICCTCTAGTGTATGCTAGAAATGGAGTGGCTGGAATAAAAGTGGCTGAATC TGATGATTTTTACATTATAGTATTACATTCCATGGATAGTTCTCAGTAGATAATCCTC THEFT TITITIAL TOTAL TOTAL TOTAL TATA ATCTTCAACTCTAGTAAGATGTCAAACTGTTTTCTAAAAGTGTTTTAATTTAACTATTAT TGTAGCTGTGGTT Gaps ; 0 Length 1453; ò

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Search completed: August 14, 2004, 19:01:36 Job time: 3749.31 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

August 14, 2004, 07:10:17; Search time 2958.17 Seconds (without alignments) 8711.839 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-082-830-98 863 1 atgggtttggtcattcaact......gctgagaccaatgatagctg 863 Title: Perfect score:

Scoring table: Sequence:

27513289 seqs, 14931090276 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1200 bp mRNA linear EST 15-MAY-2003
BX437758 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP008YB01
5-PRIME, mRNA sequence.
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with a Not1-oligo(dT) primer. Five prime end enriched,
with a Not1-oligo(dT) primer. Five prime end enriched,
the lot I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulliength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP008CA01QP1.
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DXFZp686FD11268_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DXFZp686FD11268_5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 TTTAAACAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 rergaaaggeererrraarraracaerrerergragrerargeaaarggagreer 395
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Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fsob, G., Han, M. and Wiemann, S.
EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
Unpublished (2003)
                                                                                                         /close=Invage:4419870"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="WHH MGC 88"
/note="Organ: small_intestine; Vector: pCMV-SFORT6;
Site_1: Not1; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. wiemann@dkfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.

This clone (DKFZp686FD1268) is available at the RZPD in Berlin.
Please context the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
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/note="Vector: pTriplEx2;
cDNA-collection"
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/clone="bkPzp686P11268"
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/lab_host="DH108"
                                               organism="Homo sapiens"
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xref="taxon:9606"
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/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."	Query Match 9.0%; Score 78; DB 29; Length 1392; Best Local Similarity 34.4%; Pred. No. 1.88-05; Matches 286; Conservative 0; Mismatches 540; Indels 5; Gaps 2;	Qy 11 TCATTCAACTTTAAGTTTATGAGATATATCCATGTTGAATTTTGTAGCTGTGGTTTGATG 70	Db 287 TAATITTITATAAATATAAAAATAAAATAAATATAAATTATAATTATA	71 AITITTACAITATAGATATTACATTCCATGGATAGTTCTCAGTAGATAATCCTCCTATT	4	131 GTTTAACATTTGCGTTGTCTCATTTTGACCTATTTAAACAGGCCTCTTTAAATATAC	ATTITIAATTITATTITATTITATTITTITTITTTATTAT	Oy 191 ACTICTCTGTAGTGTAGAAATGGAGTGGCTGGAATAAAAGTGGCTGAATCA 246	TITITIES IN THE TOTAL TO	Db 527 TAATAAATAAATTAATTAATTAATTAAAATTTTAAAATTTT	Qy 307 IGICAAITITGAACAGCICTITCACITACTAGCAATITAITAICAGCAACACITGITAIT 366	4.2 STATES AND THE ACT OF THE ACT	TTATATATITIAATTITATTITATTITATATTITAATATTITITAATTITITAATTITITATTITITITT 70	Db 707 TTAITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAIAATTAATTAATTAAT	Qy 487 NYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNYNY	Db 767 ATTTATTTATATATTTTTTTTTTTTTTTTTTTTTT	Qy 547 minninananananananananananananananananan	Db 827 ATTAATATATATTTTTTTTTTTTTTTTTTTTTTTTTT	QY 607 NNNNNNNNNNNNNNNNNNNNNGTGATCATATTTATGCTCATTTAAAAAAACCTGG 666	Db 887 ATTTATATTTTATATTTTATTTTTTTTTTTTTATTATATA	Qy 667 ITAAATATTICACAAATGGACAITATGATAATTATCTICCAAAATTITAATAATTITGI 726	10	OY 727 CITITICACAITITAGICTITAGCICAGCIGGAATICATIT-CIGIGIGGGGGGGA 785	Db 1007 TIAITITITITITITITITITIAIATAATATITITAATATITITITITITITITITITI 1066	Qy 786 TAAGICTITITCAIGHTTITCCCTAIGAAATAATTAITICCTUCTGTAIT 836	Db 1067 frártaatttratratratratratratratratratratrat	RESULT 5	CG753732 ON P048-4-G03.ya	ACCESSION GGF33132 vpp.grow CGF37373 GT.37978509	CG/53/32.1
OY 317 GAACAGCICTITCACTTACTAGCAATTTATTATCAGCAACACTIGITATTGTCAGACTTT 376 Dh 679 wwananwytatmayytciywwwaaacaaaaaaaaaaaaawawwwwwwqaaacaaaaaaaa	377	QY 43.7 NINNINININININININININININININININININ	Db 559 WATWWWTAAAAAAAAAAAAAAWAWWTAYCTCCCWWWTTAAAAAAAAAA	QY 497 INININININININININININININININININININ	Db 499 AWWITITITYWWAAWAITYTITTTWIWAWAAAAAAAAAAA	557 MANANANANANANANANANANANANANANANANANANAN	Db 439 МҮМНИМТИТТИАММИНТТУАНААСНҮМҮТСҮСТҮММААААААТТСТНТИТИННН 380	617	3/9 WWWWWAIAAAAWAWAWAIANIHICCICCIMIAIIIIIWAAAAAAAAAAAATIIIIAWAA 52	OY 677 CACAANTOGACATTATCATATATTATCTTCCAAAATTTTAATATTTTTT		209	OY 797 CAIGTITITICCCIAIGAGATAA 819 Db 199 TITITITIAAAAAAAAAAAAAAA 177		NOI	genomic survey sequence. ACCESSION CG757503			Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida, Neodiplogasteridae, Pristionchus.	REFERENCE 1 (bases 1 to 1392) AUTHORS Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,	Buntjer, J., van der Meuten, M. and Sommer, K.J. An integrated physical and genetic map of the nematode Pristionchus	JOURNAL Mol. Gener. Genomics 269 (5), 715-722 (2003)	12884007	Evolutionary Biology	Max.Planck-institute for Developmental blology Spemannstr. 37-39, Tuebingen D-72076, Germany	ren. 0437071601498 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de	Class: BAC ends. FEATURES Location/Qualifiers	<pre>source 11392 // Coganism="Pristionchus pacificus" // mol tyne="genomic DNA"</pre>	/strain="california" /db_xref=taxon:54126" /db_xref=taxon:54126"	/clone_lib="Ppa EcoRI BAC Library"

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1289
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1 (bases 1 to 1288)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Muulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                 CG744915 1288 bp DNA linear GSS 24-OCT-2003 P037-3-F07.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
   606 NRWINNNNNNNNNNNNNNNNNNNNGTGATCATATTTATGTTTTGCTCATTTAAAAAACCTG 665
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/db xref="ltaxon:54126"
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/note="The library was generated by a partial digest
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larity 33.5%; Pred. No. 0.00037;
Conservative 0; Mismatches 552; Indels 0;
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Max-Planck-Institute. for Developmental Biology
Max-Planck-Institute. for Developments
Tel: 00497071601371
Fax: 00497071601498
Email: ralf. sommer@tuebingen.mpg.de
Class: BAC ends.
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/organism="Pristionchus
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Strintvasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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/note="The library was generated by a partial digest of
the genemic DNA with EcoRI and cloning into the BAC
vector."
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                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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8.4%; Score 72.6; DB 29; Length 1811;
Best Local Similarity 33.2%; Pred. No. 0.00018;
Matches 276; Conservative 0; Mismatches 555; Indels 0;
                                                                                                                                                                                                                     Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                                           Mol. Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                                                                   /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                     Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
               Pristionchus pacificus
Pristionchus pacificus
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/coll line="UCD001, inbred 256"
/coll line="UCD001, inbred 256"
/clone line="Tector"
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                                                                                                                                                                                                                                                                                                                                                                                     Score 69.8; DB 28;
Pred. No. 0.00069;
); Mismatches 564;
                                                                                                    /organism="Gallus gallus"
/organism="Genomic DNA"
/strain="Red Jungle Fowl"
/db xref="texcn:9031"
/clone="CH261-13K20"
Class: BAC ends
High quality sequence start: 73
High quality sequence stop: 274.
Location/Qualifiers
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29.9%;
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Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
Marren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
Unpublished (2003)
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
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CC3015f1
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Gallus gallus
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AUTHORS
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An integrated physical and genetic map of the nematode Pristionchus
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P041-2-D06.za Ppa EcoRI BAC Library Pristionchus pacificus genomic,
genomic survey sequence.
CG747695
                                                                                                                                            666 GTTAAATATTTCACAAATCGACATTATGATATATTATCTTCCAAAATTTTAATAATTTTG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pristionchus pacificus"
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/strain="california"
/db xref="texon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
                                                                       1187 TİTTITİTİTİTINTTITITITİTİTİTİTİTİNNILİTINTITİTİTİTİTİTİTİ
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Eukaryota, Metazoa; Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601491
Email: ralf.sommer@tuebingen.mpg.de
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Loases 1 to 1380)
Srinivasan, J. Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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1. Organism="Pristionchus pacificus"
/mol type="genomic DNA"
/strain="California"
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CG748014.1 GI:37968940 GSS. genomic survey sequence

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CG748014

DEFINITION

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1 (bases 1 to 1531)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Mullen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
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Max-Planck-Institute for Developmental Biology
Max-Planck-Institute for Developmental
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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Pred. No. 0.0011;
0; Mismatches 552;
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/mol_type="genomic DNA"
/strain="California"
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Meodiplogasteridae; Pristionchus.
Srinhivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Srinhivasan, J., Sinz, W., Med Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Max-Planck Institute for Developmental Biology
Max-Planck Institute for Developmental
Tel: 072076, Germany
Tel: 00497071601371
Fax: 00497071601498
Enail: ralf:commerætuebingen.mpg.de
Class: BAC ends.
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Eukaryota, Metazoa, Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1297)
1 (bases 1 to 1297)
2 Inivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R., J.
An integrated physical and genetic map of the nematode Pristionchus
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/clone_lib="ppa_EcoRI_BAC_Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI_and cloning into the BAC
vector."
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Pred. No. 0.0013;
0; Mismatches 546; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
El: 00497071601371
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/mol type="genomic DNA"
/strain="California"
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CG758143.1 GI:37987385
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Best Local Similarity 32.1%;
Matches 258; Conservative
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Eukaryota; Mefazoa; Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 1377)
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Suntjer,J., van der Meulen,M. and Sommer,R.J.
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Pristionchus pacificus genomic,
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/mol_type="genomic DNA"
strain="dalifornia"
/db_xref="taxon:54126"
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/note="The library was generated by a partial digest the genomic DNA with EcoR! and cloning into the BAC
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
                                                                                                                                                                                                   Mol. Genet. Genomics 269 (5), 715-722 (2003) 22835951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67.2; DB 29;
Pred. No. 0.0021;
0; Mismatches 570;
                       CG749971
P044-2-E09.za Ppa EcoRI BAC Library
                                                                                                                                                                                                                                                                                                                 Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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                                                genomic survey sequence.
                                                           CG749971.1 GI:37970948
GSS.
                                                                                             Pristionchus pacificus
Pristionchus pacificus
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al Similarity 31.4%;
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/organism="Prietionchus pacificus"
/mol_type="genomic DNA"
/strain="california"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
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Eukaryota, Aratidaca, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
1 (bases 1 to 1376)
2 (chrisvasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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                                                      /organism="Pristionchus pacificus"
/mol type="genomic DNA"
/stain="California"
/db xref="Texaon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."
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Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601371
Eax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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Neodiplogasteridae, Pristionchus.
1 (Dases 1 to 1276)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntler, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
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ALIGNMENTS

Human; ss; breast specific nucleic acid; BSNA, breast cancer; mammary tumour; cytostatic; gene therapy; non-cancerous breast disorder. specific nucleic acid, BSNA #98. ВЪ ABK93492 standard; cDNA; 863 (first entry) WO200236807-A2. Homo sapiens. Human breast 23-AUG-2002 10-MAY-2002. ABK93492; ABK93492

29-OCT-2001; 2001WO-US046888. 27-OCT-2000; 2000US-0243802P. Turner LR; Liu C, Sun Y, Recipon H, Salceda S,

(DIAD-) DIADEXUS INC.

WPI; 2002-463415/49.

New breast-specific nucleic acids and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissues.

Claim 1; Page 191; 281pp; English.

The invention relates to breast specific nucleic acids (BSNA) and breast-specific polypeptides (BSP). Also included are a method for determining the BSNA in a sample, a vector comprising a BSNA, a host cell comprising the vector, a method for producing a polypeptide encoded by a BSNA, an anti-BSP antibody and a method for determining the presence of a BSP in sample. The breast-specific nucleic acids, polypeptides and compositions comprising them are useful for identifying, diagnosing, monitoring, eaginging, and treating breast cancer, mammary tumour and noncarregular in an information and included and included in the polypeptides; in gene therapy; in producing transgenic animals and the polypeptides; in gene therapy; in producing transgenic animals and

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cells; for producing engineered breast tissue for treatment and research; and as elements in an array or computer program for pattern recognition of breast disorders. The nucleic acids may be used as hybridisation probes to detect, characterise and quantify hybridising nucleic acids in, and isolate hybridising nucleic acids from, both genomic and transcript derived nucleic acid samples. The BSP protein may be used in a vaccine composition for raising an immune response against breast cancer. The present sequence is BSNA cDNA of the invention
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                                                                                                                                                                                                                                        Matches
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The invention relates to breast specific nucleic acids (BSNA) and breast-
Specific polypeptides (BSP). Also included are a method for determining
the BSNA in a sample, a vector comprising a BSNA, a host cell comprising
the vector, a method for producing a polypeptide encoded by a BSNA, an
anti-BSP antibody and a method for determining the presence of a BSP in a
sample. The breast-specific nucleic acids, polypeptides and compositions
comprising them are useful for identifying, diagnosing, monitoring,
staging, imaging, and treating breast cancer, mammary tumour and non-
comprising them are useful for identifying adjoints and antagonists of
the polypeptides; in gene therapy; in producing transgenic animals and
cells; for producing engineered breast tissue, for identifying and
cells; for producing engineered breast tissue for treatment and research;
and as elements in an array or computer program for pattern recognition
of breast disorders. The nucleic acids may be used as hybridisation
and isolate hybridising nucleic acids from, both genomic and transcript-
derived nucleic acid samples. The BSP protein may be used in a vaccine
composition for raising an immune response against breast cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TCCTCCTATTGTTTAACATTTGCGTTGCTTCTCATTTTGACCTATTTTAAACAGGCCTCT 180
                                                                                                                                                                                                                                           Human; ss; breast specific nucleic acid; BSNA; breast cancer; mammary tumour; cytostatic; gene therapy; non-cancerous breast disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New breast-specific nucleic acids and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging, and treatibreast cancer and non-cancerous disease states in breast tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 392;
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Pred. No. 3.7e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is BSNA cDNA of the invention
                                                                                                                                                                                                       Human breast specific nucleic acid, BSNA #97.
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841 GTAGCTGAGACCAATGATAGCTG 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu
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                                                                                           ВР.
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                                                                                           ABK93491 standard; cDNA; 392
                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001; 2001WO-US046888.
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                                                                                                                                                                   (first entry)
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Best Local Simi
Matches 392;
                                                                                                                             ABK93491;
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                                                     RESULT 2
ABK93491
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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                              ATTATATGTCAATTTTGAACAGCTCTTTCACTTACTAGCAATTTATTATCAGCAACTT
                                                                                                                                ATTATATGTCAATTTTGAACAGCTCTTTCACTTACTAGCAATTTATTATCAGCAACTT
                                                                                   GAATCATCTTCAACTCTAGTAAGATGTCAAACTGTTTTCTAAAAGTGTTTTATTTTAACT
                                           TTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGAATAAAAATAAAAGTGGCT
                                                                        GAATCATCTTCAACTCTAGTAAGATGTCAAACTGTTTTCTAAAAGTGTTTTATTTTAACT
                               TTAAATATACACTTCTCTGTAGTGTATGCTAGAATGGAGTGGCTGGAATAAAAGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of breast
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                                                                                                                                                                                                                                                                                           breast cancer expressed polynucleotide 18497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as a marker for the diagnosis
                                                                                                                                                                                                                                                                                                                 breast cancer; cell marker; cytostatic;
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14-MAR-2000; 2000US-0189167P.
24-MAR-2000; 2000US-0192099P.
25-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
09-UUN-2000; 2000US-021315P.
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ID AAL26040 standard; cDNA; 229
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                                                                                                                                                                                                                                                                       (first entry)
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Score 89.8; DB 4; Length 229; Pred. No. 1.6e-09; 0; Mismatches 2; Indels (

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91; Conservative

Query Match Best Local Similarity Matches 91; Conserv

10.4%; 97.8%;

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                                The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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AAACAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Human breast cancer expressed polynucleotide 9295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; breast cancer; cell marker; cytostatic;
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                                                                                                                                 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA
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14-WAR-2000; 2000US-0189167P.
24-WAR-2000; 2000US-019209P.
29-WAR-2000; 2000US-0193480P.
15-WAY-2000; 2000US-0205230P.
09-UJN-2000; 2000US-021115P.
25-JUL-2000; 2000US-021115P.
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97.8%;
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les 91; Conservative
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Homo sapiens

AAL17847;

AAL17847/

10-JAN-2001; 14-JAN-2000;

19-JUL-2001

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The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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Human; breast cancer; cell marker; cytostatic; ss.
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                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                               Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1823; 3695pp; English.
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14-WAR-2000; 2000US-0189167P.
24-WAR-2000; 2000US-01999P.
29-WAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0205230P.
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25-JUL-2000; 2000US-0220534P.
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97.8%;
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                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 256 BP; 72 A; 56 C; 57 G; 71 T; 0 U; 0 Other;
                                                                                                                                              Human breast cancer expressed polynucleotide 10304
                                                                                                                                                                                  Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 261
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                                AAL17847 standard; cDNA; 256 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2000; 2000US-0193480P
15-MAY-2000; 2000US-0205230P
09-UTN-2000; 2000US-021315P
25-UTL-2000; 2000US-0220534P
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                                                                                                        07-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang Y,
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Lillie J,

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Gaps

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Indels

144

10-JAN-2001; 2001WO-US000798

Human breast cancer expressed polynucleotide 10227.

(first entry)

07-DEC-2001

AAL17770

RESULT

AAL17770
ID AAL:
XX
AC AAL:
XX
DT 07-1
XX
DE Hum

229 114

g ò g

8

Query Match Best Local 8

Matches

19-JUL-2001.

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213 AAAATGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGA 154
                                                                                                                                     The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a parient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                       diagnosis of breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                 Length 298;
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                                                                                                                                                                                                                                                                                                                          73 G; 78 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; breast cancer; cell marker; cytostatic; ss.
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Pred. No. 1.7e-09;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 261
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                                                                     New peptide useful as a marker for the
Steinmann
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                                                                                                        English.
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24-MAR-2000; 2000US-0199167P.
29-MAR-2000; 2000US-019309P.
29-MAR-2000; 2000US-0193480P.
15-MAY-2000; 2000US-0208330P.
09-UIN-2000; 2000US-021315P.
25-UIL-2000; 2000US-0220534P.
                                                                                                                                                                                                                                                                                                                              Sequence 298 BP; 77 A; 69 C;
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1 Similarity 97.8%;
91; Conservative
                                                                                                          Claim 1; Page 596; 3695pp;
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Wang Y,
                                    WPI; 2001-451856/48.
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Χu Υ,
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Lillie J,
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Best Local S:
Matches 91
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                                                                                                                                                                                                                                                                                                                          The invention relates to human breast cancer expressed polymucleotides (AA107544-AA126789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising trearing and potentially preventing breast cancer. The polymucleotides and polypeptides are also useful for isolating compounds with cytostatic
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Pred. No. 1.7e-09;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 189
                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                Steinmann K;
                                                                                                                                                                                                                                                                                           Claim 1; Page 583; 3695pp; English.
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                               24-MAR-2000, 2000US-019209997-29-MAR-2000, 2000US-0193480P.
15-MAY-2000, 2000US-02030P-09-UUN-2000, 2000US-021315P-25-UUL-2000, 2000US-0220534P-
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97.88;
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2000US-0192099P.
2000US-0193480P.
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2000US-0176077P.
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24-MAR-2000;
29-MAR-2000;
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14-JAN-2000;
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91;
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Query Match Matches

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           The invention relates to human breast cancer expressed polymucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                         Gaps
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                                                                                                                                                        Length 317;
                                                                                                                                                                                       2; Indels
                                                                                                                          Sequence 317 BP; 86 A; 69 C; 77 G; 85 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed polynucleotide 1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                          Score 89.8; DB 4;
Pred. No. 1.7e-09;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                   199 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 231
                                                                                                                                                                                                                                                                                 229 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 261
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2000US-0192099P.
2000US-0193480P.
2000US-0205230P.
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ilarity 97.8%;
Conservative
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                                                                                                                                                                          Similarity
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15-MAY-2000; 2
09-JUN-2000; 2
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24-MAR-2000;
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Best Local S:
Matches 91
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G; 86 T; 0 U; 0 Other;

Sequence 332 BP; 86 A; 75 C; 85

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                                                                                                    169 AAACAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGA 228
                                                                                                                                                 154 AAAATGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
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                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85; DB 4; Lengtn oz.,
Pred. No. 1.88-08;
                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human breast cancer expressed polynucleotide 14436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; breast cancer; cell marker; cytostatic; ss.
  Score 89.8; DB 4;
Pred. No. 1.7e-09;
0; Mismatches 2
                                                                                                                                                                                                   229 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 261
                                                                                                                                                                                                                                                214 ATAAAAGIGGCIGAATCAICTICAACTCTAGTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide useful as a marker for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y, Steinmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 2592; 3695pp; English.
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2000US-0189167P.
2000US-0192099P.
     10.4%;
                                                                                                                                                                                                                                                                                                                                                                               AAL21979 standard; cDNA; 525
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2000US-0211315P.
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                                                       Conservative
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Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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265 AAAATGGCCTCTTTAAANANACACTTCTCCTGTAGTGTATGCTANAAATGGAGTGGCTGG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiac damage, inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; osophageal cancer; ds; tumour; immunostimulant; cardiat; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of certain markers and the cancerous state of breast cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides are also useful for isolating compounds with cytostatic activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71.6; DB 4; Length 534;
Pred. No. 1.1e-05;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 534 BP; 119 A; 121 C; 119 G; 142 T; 0 U; 33 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene regulation-associated gene oligonucleotide #49.
                                                               Human; breast cancer; cell marker; cytostatic; ss.
                    breast cancer expressed polynucleotide 5566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AATAAAAGTGGCTGAATCATCCTCNACTTAGTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 AATAAAAGTGGCTGAATCATCTTCAACTCTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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24-MAR-2000; 2000US-0192099P.
29-MAR-2000; 2000US-0193480P.
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09-JUN-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0220534P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu Y, Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                WO200151628-A2
                                                                                                          Homo sapiens.
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                                                                                                                                                                                         19-JUL-2001
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                        Human
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human breast cancer expressed polynucleotides afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially-preventing breast cancer. The polynucleotides and encoded polypeptides are potential anxhers for potentially-preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
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Pred. No. 5.1e-07;
0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 248 BP; 61 A; 61 C; 61 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                           cell marker, cytostatic; ss
                                                                                                                                                                                                                                  Human breast cancer expressed polynucleotide 752.
327 ATAAAAGTGGCTGAATCATCCTCAACTTTAGTA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAAAGIGGCIGAAICAICIICAACICIAGIA 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 208; 3695pp; English.
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2000US-0205230P.
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                                                                                                   AAL08295 standard; cDNA; 248
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24-MAR-2000; 2000US-0192099P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90; Conservative
                                                                                                                                                                                                                                                                             breast cancer;
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15-MAY-2000;

29-MAR-2000; 09-JUN-2000;

25-JUL-2000;

Lillie J,

07-DEC-2001

AAL13109;

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AAL13109,

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169

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Query Match Best Local S **Jatches** 130

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14-JAN-2000;

Homo sapiens

19-JUL-2001

07-DEC-2001

AAL08295;

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AAL08295

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TITITAAATTITAATTAGTTAGTITITITTGTTTAAAGTTITTAAAATTTTTTGAAGAA 5600
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                                       Human; immune system disease; cytosine methylation; antiasthmatic; antiansemic; cytosines inociropic; antiansemic; cytostatic; nociropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antifammatory; cancer; eye disease; arterioscleroals; anaemia; antimitalmamatory; cancer; eye disease; atterioscleroals; anaemia; altheimer* a disease; ALDS; epilepsy; neurofibromatosis; heumatodia arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for
                                                                                                                                                                                                                                                                  5601 ATTTGTATGATATATTTTTTTTTTTTGGTTAATTTGTTATATTTTGTTTAAATT
                                                                                                                                                                                                                                                                                                                                                       5721 TITITITITIAAGTITIAGTITIAATTATTATTTTTTTAAAAGTITTTTTTTGATTATAAA
                                                                                    NNNNNNNGTGATCATATTTATGTTTTTGCTCATTTAAAAAAACCTGGTTAAATATTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAICGACATTAIGATAITAICTICCAAAAITITAAIAAITITGICTITITICACAIT
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2000DE-01043826.
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                                                                                    5481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNB sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, whence syndrome, asthma, then syndrome, asthma pare regulation and is associated with the human gene regulation-associated present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.8%; Score 67.6; DB 6; Length 6062; 32.8%; Pred. No. 9.6e-05; ative 0; Mismatches 552; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 50; 26pp; English
                                                                                                                                                                                                                                                                                                                                    Berlin
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20000E-01019173.
20000E-01032529.
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70; Conservative
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                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
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                                          WO200177375-A2
                                                                                                                                                                         06-APR-2000;
07-APR-2000;
30-JUN-2000;
  Homo sapiens
                                                                                                                                 06-APR-2001;
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Matches 27
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid retwaemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, remanatoid arthritis, psociasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6195 BP; 1636 A; 57 C; 1209 G; 3293 T; 0 U; 0 Other;
                                                                                 Claim 1; SEQ ID NO 564; 32pp + Sequence Listing; German
                             methylation
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Length 6195;

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TTAAGTTTTATGAGATATATCCATGTTGAATTTTTGTAGCTGTGGGTTTGATGTTTTTACAT
                                          3391 TIATATITITITATITATITATITATICATGAATATITAGGITAATITITATATITIGIT
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Search completed: August 14, 2004, 19:13:42 Job time : 437.526 secs
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August 14, 2004, 19:13:54; Search time 490.203 Seconds (without alignments) 8638.053 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					COLUMNIA	
Result No.	Score	% Query Match	% Query Match Length DB 1	BG	Ç	Description
				1		
М	630	73.0	863	15	US-10-082-830-98	Sequence 98, Appl
7	392	45.4	392	15	US-10-082-830-97	Sequence 97, Appl
m	91.2	10.6	1017	15	US-10-198-846-11216	Sequence 11216, A
4	80.00	10.4	390	15	US-10-198-846-10053	Sequence 10053, A
S	89.8	10.4	393	15	US-10-198-846-887	Sequence 887, App
9 U	89.8	10.4	441	15	US-10-198-846-2119	Sequence 2119, Ap
7	89.8	10.4	481	15	US-10-198-846-2043	Sequence 2043, Ap
დ ე	71.6	8.3	1015		US-10-198-846-4377	Sequence 4377, Ap
თ	67.6	7.8	6062		US-10-221-613-50	Sequence 50, Appl
10	66.2	7.7	6195	15	US-10-311-455-564	Sequence 564, App
c 11	64.4	7.5	1214	13	US-10-424-599-102083	Sequence 102083,
12	63.6	7.4	3673778	=======================================	US-10-312-841-1	Sequence 1, Appli
13	62.8	7.3	7128		_	Sequence 1532, Ap
14	62.8	7.3	40324	17	US-10-433-793-180	Sequence 180, App

equence 470, equence 470, equence 470, equence 105, equence 107, equence 107, equence 23, equence 23, equence 22, equence 22, equence 23, equence 240, equence 260, equence 260, equence 260, equence 260, equence 11	sednence s, Appli
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ALIGNMENTS

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Sequence 98, Application US/10082830

Publication No. US20030077604A1

GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Salceda, Susana
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Genes and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0249
CURRENT APPLICATION NUMBER: 05/10/082,830
CURRENT APPLICATION NUMBER: 60/243,802
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-27
NUMBER OF SEQ ID NOS: 22.
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73.0%; Score 630; DB 15; I
Best Local Similarity 100.0%; Pred. No. 3.9e-119;
Matches 863; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (395)..(627)
; OTHER INFORMATION: a, c, g or t
US-10-082-830-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
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APPLICANT: Lillie, James
APPLICANT: Arongyao
APPLICANT: Wangy Youzhan
APPLICANT: Wangy Youzhan
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR PRIOR PELLOR DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14094
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ-ID NO 11216
LENGTH: 1017
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                                                                                                                                                                                                                                                                                                                                                                             Length 392;
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
45.4%; Score 392; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 392; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred. ]
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PRIOR FILING DATE: 2000-10-27

NUMBER OF SEQ ID NOS: 282

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 97

LENGTH: 392

TYPE: DNA

TYPE: DNA

US-10-082-830-97
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) LOCATION: 1017

) OTHER INFORMATION: n = A,T,C our our of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-198-846-11216
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US-10-082-330-97
US-10-082-330-97
US-10-082-330-97
Squence 97, Application US/10082830
Publication No. US20030077604A1
GENERAL INFORMATION:
APPLICANT: Salceda. Susana
APPLICANT: Aslceda. Susana
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
ITILE OF INVENTION: Genes and Proteins
FILE REFERENCE: DEX-0249
CURRENT APPLICATION UNDERS: US/10/082,830
CURRENT APPLICATION NUMBER: 80/243,802
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                 TGGTTTGATGATTTTTACATTATATATAGTATTACATTCCATGGATAGTTCTCAGTAGATAA 120
                                                                 TGGTTTGATGATTTTTACATTATATAGTATTACATTCCATGGATAGTTCTCAGGATAAA
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Gaps

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Indels

Length 393;

DB 15; 2;

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178 AAAATGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGA 237
                                                                                                                                                                                                                                                                                                                                                                                                                            238 ATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 270
                                                                                                                                                                                                                                                                                                                                                                                            229 ATAAAAGIGGCIGAAICAICTICAACICTAGIA 261
                                                                                                                                                                                                         Query Match
10.4%; Score 89.8; DB 1
Best Local Similarity 97.8%; Pred. No. 8e-09;
Matches 91; Conservative 0; Mismatches
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US-10-198-846-2043
is Sequence 2043, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
    APPLICANT: Lillie, James
; APPLICANT: Wang, Youghan
; APPLICANT: Steinmann, Kathleen
                                                                                                                                                                                                                                                                                                      169 AAACAGGCCTCTTTAAATATACACTT
                                                                                     NAME/KEY: misc_feature

LOCATION: 393

CTHER INFORMATION: n = A,T,C or G

US-10-198-846-887
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1 LOCATION: 3, 53

2 OTHER INFORMATION: n = A,T,C or G

US-10-198-846-2119
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Best Local Similarity 97.83
Matches 91; Conservative
LENGTH: 393
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-198-846-2119/c
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                                              166 TTTAAACAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AAACAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAATGGAGTGGCTGGA 228
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APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhao
APPLICANT: Wang, Youzhao
APPLICANT: Wang, Youzhao
APPLICANT: Wang, Youzhao
APPLICANT: Steinmann, Kathleen
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
FRIOR PRILING DATE: 2002-07-18
FRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                         367 TCTGAAAAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGGGCT
  Gaps
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PREVENTION, AND
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    3; Indels
                                                                                                                                                                                                                                                                                  Sequence 10053, Application US/10198846

Sequence 10053, Application US/10198846

Bublication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Wangyao

APPLICANT: Stainmann, Karblen

TITLE OF INVENTION: POWIL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, FREN

TITLE OF INVENTION: THERAPY OF BREAST CANCER

TITLE OF INVENTION: UNMERR: US/10/198,846

CURRENT APPLICATION NUMBER: 06/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ. ID NOS: 14084

SOFIWARE: FASEUSED for Windows Version 4.0

LENGTH. 390

"LENGTH. 390
                                                                                                                                       226 GGAATAAAAGIGGCIGAATCAICTICAACICTAGIA 261
                                                                                                                                                                    427 GGAATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.4%; Score 89.8; DB 15;
Best Local Similarity 97.8%; Pred. No. 7.9e-09;
Matches 91; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 ATAMAAGTGGCTGAATCATCTTCAACTCTAGTA 261
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 887, Application US/10198846; Publication No. US20030099974A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature; LOCATION: 386, 387, 388, 389, 390; OTHER INFORMATION: n = A,T,C or G US-10-198-846-10053
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0
  93; Conservative
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ORGANISM: Homo sapiens
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  Matches
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216 AAAATGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCTAGAAATGGAGTGGCTGGA 157
Sequence 2119, Application US/10198846

Publication No. US2003009974A1

General Invermanton:

General Invermanton:

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Lillie, James

APPLICANT: Wangy Youchen

TILLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TILLE OF INVENTION: THERAPY OF BEREAST CANCER

TILLE REFERENCE: MRI-049

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICANTON NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR PRIOR TILING DATE: 2001-07-18

SOFTWARE: FEALENCE THOUGH OF SEQ ID NOS: 14084

SOFTWARE: FEALENCE THOUGH OF SEQ ID NOS: 14084

SOFTWARE: FEALENCE THOUGH OF SEQ ID NOS: 14084
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Pred. No. 8.3e-09;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Squence 4377, Application US/10198846
; Squence 4377, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: NOVEL GENES,
TITLE OF INVENTION: TOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-649
CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2001-07-18
; PRIOR PILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SCFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4377
; LENGTH 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188, 191,
442, 459,
585, 602,
775
      AND METHODS
PREVENTION, AND
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LOCATION: 5, 7, 11, 14, 15, 16, 18, 19, 20, 22, 23, 27, 29, 31, 35, LOCATION: 5, 7, 11, 14, 15, 16, 18, 19, 50, 53, 54, 55, 56, 57, 59, LOCATION: 61, 62, 63, 65, 67, 69, 73, 75, 81, 82, 83, 84, 85, 86, LOCATION: 87, 89, 90, 93, 94, 96, 97, 98, 99, 103, 106, 108, 109, LOCATION: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.4%; Score 89.8; DB 15; Length 481;
Best Local Similarity 97.8%; Pred. No. 8.6e-09;
Matches 91; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                            93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186,
401,
569,
758,
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE; FILE EPPERBERS. MILOGO ENTRY OF BREAST CANCER FILE EPPERBERS: MILOGO ENTRY OF BREAST CANCER CURRENT PELLING DATE: 2002-07-18 PRIOR APPLICATION NUMBER: 60/306,220 PRIOR APPLICATION NUMBER: 60/306,220 PRIOR FILING DATE: 2001-07-18 NUMBER OF SEQ ID NOS: 14084 SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0 LENGTH: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175,
399,
516,
755,
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374,
515,
744,
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308,
502,
715,
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

; LOCATION: 2, 3, 4, 5, 13, 14, 16, 17,

; LOCATION: 333, 464; 478

; OTHER INFRAITON: n = A,T,C or G

US-10-198-846-2043
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 111, 113, 121, 124, 130, 13
LOCATION: 193, 212, 256, 292, 298, 30
LOCATION: 642, 472, 495, 497, 498, 50
LOCATION: 648, 641, 655, 656, 695, 71
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
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US-10-198-846-4377/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5302 AAGTGGGTATTAAT-TCGTTTTGTAAATTAGAAATATGGGTATTTATTTAGTTCGT 5360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 AAAATGGCCTCTTTAAANANACACTTCTCCTGTAGTGTATGCTANAAATGGAGTGGCTGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WS-10-21 613-50

WS-10-221 613-50

Sequence 50, Application US/10221613

Publication US/2040029123A1

BENERAL INFORMATION:

APPLICANT: DIEPENBROCK, Christian

APPLICANT: DIEPENBROCK, Christian

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 AAACAGGCCTCTTTAAATATACACTTCT-CTGTAGTGTATGCTAGAAATGGAGTGGCTGG
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                          921,
963,
                                      908,
958,
                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                    Length 1015;
                                      907,
                                                                                                                                                                                                                                                                                8.3%; Score 71.6; DB 15; Length
90.4%; Pred. No. 6e-05;
lve 0; Mismatches 8; Indels
                                          905,
951,
                                              880,
940,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 AATAAAAGTGGCTGAATCATCCTCNACTTTAGTA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AATAAAAGTGGCTGAATCATCTTCAACTCTAGTA 261
                                              866,
939,
                                              854,
; NAME/KEY: misc_feature
; LOCATION: 808, 809, 810, 842, 847,
; LOCATION: 924, 925, 926, 933, 934,
; LOCATION: 969, 994, 996, 1013
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-4377
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                                                                                                                                                                                                                                                                                                                               90.4%;
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Best Local Similarity 90.4
Matches 85, Conservative
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Best Local Similarity 32.8
Matches 270; Conservative
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NUMBER OF SEQ ID NOS: 428
SEQ ID NO 50
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Sequence 102083, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF THE REPERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 102083
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                            TATATAGTATTACATT-CCATGGATAGTTCTCAGTAGATAATCCTCCTATTGTTTAACAT
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Sequence 564, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: DIEDENBROCK, Christian

APPLICANT: BERLIN, Kurt

ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ

ITILE OF INVENTION: OYCOSINE methylation

FILE REFERENCE: 5013.104

FILE REPERENCE: 2013.104

CURRENT APPLICATION NUMBER: PCT/EP01/07537

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01
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   Gaps
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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llarity 34.2%; Pred. No. 0.0015;
Conservative 0; Mismatches 511;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 269; Conserval
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US-10-311-455-564
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LENGTH: 6195
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TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 29.3%;
Matches 171; Conservative
                                                                                                                                                                                           ) NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
                                                                                                                        LENGTH: 3673778
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                                                                                                                        Query Match 7.5%; Score 64.4; DB 13; Best Local Similarity 29.5%; Pred. No. 0.0019; Matches 245; Conservative 0; Mismatches 586;
                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_63198C.1
US-10-424-599-102083
                                                                  all n locations
                                                                   at
                                          NAME/KEY: unsure
LOCATION: (1)..(1214)
OTHER INFORMATION: unsure
          TYPE: DNA ORGANISM: Glycine max
LENGTH: 1214
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RESULT 12

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Sequence 1, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Epigenomics AC
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT APPLICATION NUMBER: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3673778;
                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 0.062;
0; Mismatches 412;
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Sequence 1532, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian
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37936 ATTTTTTTTAATTTAAAGTATATATTTÄTTTTATTÄTGTTTTTAATGAAATTTAATTTG 37995
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US-10-433-793-180
IS-10-433-793-180
Sequence 180, Application US/10433793
Sequence 180, DS20040142334A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Diagnose von mit Anglogenese assoziierten Krankheiten
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT APPLICATION DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 180
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Pred. No. 0.016;
0; Mismatches 570;
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; OTHER INFORMATION: chemically treated genomic DNA
US-10-433-793-180
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Best Local Similarity 31.7%;
Matches 265; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Length 7128;
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Pred. No. 0.0081;
0; Mismatches 570;
                 TITLE OF INVENTION: Diagnosis of Diseases As TITLE OF INVENTION: Cytosine methylation FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PGT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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Similarity 31.7%;
65; Conservative (
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US-10-311-455-1532
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Best Local Simi
Matches 265;
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Publication No. US203030143606A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OLEX, Alexander
APPLICANT: DESPENSECK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
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SPRIOR FILING DATE: 2000-09-01
SPRIOR FILING DATE: 2000-09-01
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                                                                                                                                        TITIGECTITITICACATITIAGICITIAGCICAGCIGGAATICATITCIGIGIGGIG
                                                        ACCTGGTTAAATATTTCACAAATCGACATTATGATATATTATCTTCCAAAATTTTAATAA
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Pred. No. 0.026;
0; Mismatches 547; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 33.2%;
Matches 275; Conservative
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Sequence 39, 7
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/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-10-10

Sequence 2, Application US/10204708

Patent NO. 6677731

SEQUENCE INFORMATION:

APPLICANT: CLEX, Alexander

APPLICANT: DISPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BEELIN, Kurt

ITILE OF INVENTION: DASSESSING DNA Methylation

FILE REPERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10013529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR ELING DATE: 2000-06-30

PRIOR ELING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98
                         Sequence 11, Appl
Sequence 15, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 3, Appl
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Best Local Similarity 30.7%; Pred. No. 0.00017;
Matches 231; Conservative 0; Mismatches 522;
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US-08-855-629-11
US-10-204-708-75
US-10-204-708-45
US-10-204-708-45
US-08-910-988-1
US-08-916-421B-1
US-08-916-421B-1
US-08-213-4188-3
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ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR PRILOR DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PRILOR DATE: 2000-04-06
PRIOR PRILOR DATE: 2000-04-07
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PRIOR PILING DATE: 2000-03-01
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                                                               ATAGITATITATIAIAAITITIGAITITITITITITAAGAGITITITAAAIGITATITGITT 2698
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                               AAAGIGTTTTATTTAACTATTATATGTCAATTTTGAACAGCTCTTTCACTTACTAGCAA
                                                                                                                                                                                                                    2819 TITITIATGGTATATATATATTGTAGTGTTTTGAAAGGTAATTAATATTAGGTGTTTTATA
                                                                                           TITATIATCAGCAACACTIGITATTGTCAGACTTTTAAGTTTTCATTCACTGGNNNNNNN
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
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ORGANISM: Artificial Sequence
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Best, Local Similarity
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LENGTH: 19513
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Length 19513;

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                                                                                                                                                              TITIGACCIATITITAAACAGGCCICTITAAATATACACTICTCTGTAGTGTATGCTAGAA
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APPLICANT: PIEPENBROCK, CA
APPLICANT: BERLIN, Kurt
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APPLICANT: OLEK, Alexander
APPLICANT: PIEBPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
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PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10013529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-10
NUMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 98
LENGTH: 5535
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FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2003-05-06

PRIOR PILING DATE: 2003-05-06

PRIOR FILING DATE: 2000-04-06

PRIOR PLING DATE: 2000-04-06

PRIOR PLING DATE: 2000-04-07

PRIOR PLING DATE: 2000-04-07

PRIOR PLING DATE: 2000-04-07

PRIOR PLING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

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; Patent No. 6410712

; GENERAL INFORMATION:

APPLICANT: Berglind Ran Olafsdottir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 27.6%;
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-426-290-1/c
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Sequence 1, Application US/09351794A
Fatent No. 6641815
GENERAL INFORMATION:
APPLICANT: DUFFY, PATRICK E.
APPLICANT: OCKENHOUSE, CHRISTIAN F.
TITLE OF INVENTION: SEQUESTRIN
FITE REFERENCE: 38644-175519
CURRENT FILING DATE: 1999-07-13
PRIOR PILING DATE: 1995-11-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SENGTH: 1956
ATTORNEY/AGENT INCOLLAR NAME: Moran, John
REGIGSTRATION UNDBER: 26,313
REFERENCE/DOCKET NUMBER:
TELEFONNE: (301) 619-2065
TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERSTICS:
LENGTH: 1956 base pairs
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.5%;
Matches 138; Conservative
                                                                                                                                                                                                                                                    Linear
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US-09-351-794A-1/c
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Pred. No. 0.044;
0; Mismatches 68; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TCATTCAACTTTAAGTTTATGAGATATATCCATGTTGAA
      APPLICANT: Jeffrey Gulcher
FILE OF INVENTION: HUMBAN NARCOLEPSY GENE
FILE REFERENCE: 2345,2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
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STREET: USA MRMC - MCMR-JA
CITY: FORT DETRICK, FREDERICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER: FLORM:
MEDIUM TYRE: FLORM:
MEDIUM TYRE: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsofte Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,896B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTRIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-559-896B-1/c
; Sequence 1, Application US/08559896B
; Patent No. 6310046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.2%;
Matches 100; Conservative
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION WIMBER:
FILING DATE:
                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                   LENGTH: 168575
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; LOCATION: (1
US-09-426-290-1
                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                NAME/KEY
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1120 TITCATACCTTGCTTCTGATCCATTCTAATTCTTAATTCTTTATAAAGTCTATCGATTT 1061
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                                                                                                                                                                                                                                               940 GATCTTTATCCATTTTATTTATTTTCTCTTTTTCAATTTTGGGAATTTTTCTCTATGAA 881
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                                                             Gaps
                                                                .
0
   DB 4; Length 1956;
Score 48; DB 4; Length 195
Pred. No. 0.02;
0; Mismatches 383; Indels
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NAME/KEY: misc feature
LOCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018 gene
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OTHER INFORMATION: 5'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 1108..1289
OTHER INFORMATION: exon A g35018 gene
PRICR FILING DATE: 1999-07-29
PRICR APPLICATION NUMBER: US 60/162,288
PRICR FILING DATE: 1999-10-28
PRICR APPLICATION NUMBER: US 09/416,384
PRICR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent.pm
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LOCATION: 65505..65853
OTHER INFORMATION: exon G 935018 gene
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LOCATION: 201188..201234
OTHER INFORMATION: exon S g35030 gene
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OTHER INFORMATION: exon V 935030 gene
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LOCATION: 14877...14920
OTHER INFORMATION: exon B g35018 gene
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OTHER INFORMATION: exon T 935030 gene
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OTHER INFORMATION: exon C 935018 gene
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LOCATION: 29967..30282
JTHER INFORMATION: exon E 935018 gene
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OTHER INFORMATION: exon F g35018 gene
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LOCATION: 18778..18862
DTHER INFORMATION: exon Bbis 935018
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LOCATION: 215702..215746
OTHER INFORMATION: exon U g35030
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THER INFORMATION: exon g35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                 LENGTH: 319608
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                                                                                                                                                                                                                                            TYPE: DNA
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APPLICANT: COREN, Dantel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Dernard
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Dernard
APPLICANT: Bihain, Dernard
APPLICANT: Bihain, Dernard
APPLICANT: Bihain, Dernard
APPLICANT: Bihain, Dernard
APPLICANT: Bihain, Dernard
APPLICANT: Bougueleret, Lydie
APPLICANTON: SCHIZOPRRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENET: 047-0430
CURRENT APPLICATION NUMBER: US 60/126, 903
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
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PRIOR FILING DATE: 1999-07-29
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                                                                                                                                                                                                                                                                                                                  305 TATGTCAATTTTGAACAGCTCTTTCACTTACTAGCAATTTATTATCAGCAACACTTGTTA 364
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                                                                                                                5.6%; Score 48; DB 4; Length 1956;
26.5%; Pred. No. 0.02;
tive 0; Mismatches 383; Indels
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; Sequence 1, Application US/09539333D
; Patent No. 6476208
                  ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-351-794A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 11ya
                                                                                                                      Query Match
Best Local Similarity 26.55
Matches 138; Conservative
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us-10-082-830-98.rni

VAME/KEY: exon LOCATION: 240528..240617 OTHER INFORMATION: exon M1069 complement g34872 gene VAME/KEY: exon VAME/KEY: 240528..240596 COCATION: 240528..240596 OTHER INFORMATION: exon M1090 complement g34872 gene NAME/KEY: exon LOCATION: 215819..215975 OTHER INFORMATION: exon Rbis complement g34872 gene NAME/KEY: exon LOCATION: 216661..216952 OTHER INFORMATION: exon Qbis complement g34872 gene AAME/KEY: exon COCATION: 231272..231412 DTHER INFORMATION: exon Obis complement g34872 gene NAME/KEY: exon LOCATION: 240528..240569 OTHER INFORMATION: exon M1117 complement g34872 gene NAME/KEY: exon OCATION: 237406..237428 OTHER INFORMATION: exon Nbis complement g34872 gene LOCATION: 213818..215818 OTHER INFORMATION: 3'regulatory region g34872 gene NAME/KEY: exon LOCATION: 217027..217061 OTHER INFORMATION: exon Q1 complement g34872 gene IAME/KEY: exon JOCATION: 231787..231880 THER INFORMATION: exon O2 complement g34872 gene AAME/KEY: exon JOCATION: 231870..231879 OTHER INFORMATION: exon O1 complement g34872 gene TAME/KEY: exon JOCATION: 239719..239807 THER INFORMATION: exon N2 complement g34872 gene LOCATION: 215819..215941 OTHER INFORMATION: exon R complement 934872 gene NAME/KEY: exon LOCATION: 216661..217061 OTHER INFORMATION: exon Q complement g34872 gene NAME/KEY: exon LCCATION: 229447..229742 OTHER INFORMATION: exon X complement g34872 gene NAME/KEY: exon LOCATION: 230408..230721 OTHER INFORMATION: exon P complement g34872 gene ARME/KEY: exon ACCATION: 234174..234321 OTHER INFORMATION: exon O complement g34872 gene RATURE: NAME/KEY: exon LOCATION: 239719..239853 OTHER INFORMATION: exon N complement g34872 gene FEATURE: NAME/KEY: exon LOCATION: 240528..240644

Sequence 1, Application US/09679409

Sequence 1, Application US/09679409

Patent No. 6555316

GENERAL INPORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Chimakov, Ilya

APPLICANT: Daniel

CURRENT APPLICATION NUMBER: 09/916/39,333

PRIOR FILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

NUMBER OF SEQ ID NOS: 134

SEQ ID NO 1

ENGTHARE: Patent.pm

SEQ ID NO 1

ENGTHARE: Patent.pm 15563 15562 AGAATTCCAFTCTAFGGAFATACCAAAATCCAFCCATTCTACTGTTGATTGACATTTGGG 15503 ٠<u>.</u> 82 15622 Trridakirircarccardrideressererakaraaraareracrentriraacrererer 86 AGTATTACATTCCATGGATAGTTCTCAGTAGAT-AATCCTCCTATTGTTTAACATTTGCG 27 ITATGAGATATATCCATGTTGAATTTTGTAGCTGTGGTTTGATGATTTTTAC-ATTATAT 2; Gaps Query Match 5.4%; Score 46.6; DB 4; Length 319608; Best Local Similarity 65.8%; Pred. No. 0.12; Matches 98; Conservative 0; Mismatches 49; Indels 2; NAME/KEY: exon LOCATION: 240528..240824 OTHER INFORMATION: exon M862 complement g34872 gene LOCATION: 240528..240994 OTHER INFORMATION: exon M692 complement g34872 gene FEATURE:
NAME/KEY: misc feature
LOCATION: 241656..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
PRATURE:
NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
FEATURE:
NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon M31 complement g34872 gene OTHER INFORMATION: exon MS2 complement g34872 gene FEATURE: 15502 chruricccarriggagcrarrccaara 15474 145 TIGCTICTCATTITGACCIATTIAAACA 173 NAME/KEY: exon LOCATION: 292653..292841 NAME/KEY: exon LOCATION: 2405; RESULT 9 US-09-679-409-1/c FEATURE: ð d рр ò ö

TYPE: DNA ORGANISM: Homo sapiens FEATURE:

NAME/KEY: allele
LOCATION: 65485
OTHER INFORMATION: 8-128-33 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 95396
OTHER INFORMATION: 99-31960-363 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 107281
OTHER INFORMATION: 99-24656-260 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 160640
OTHER INFORMATION: 99-24639-163 : polymorphic base A or C : polymorphic base A or C : polymorphic base A or T 99-7652-162 : polymorphic base A or G AME/KEY: allele OCATION: 8316 THER INFORMATION: 99-27943-150 : polymorphic base G or AME/KEY: allele OCATION: 21672 : polymorphic base G or NAME/KEY: misc feature LOCATION: 199122..201122 OTHER INFORMATION: 5'regulatory region AME/KEY: misc feature OCATION: 247803..249803 THER INFORMATION: 3'regulatory region /KEY: allele IION: 160876 RINFORMATION: 99-24634-108 INFORMATION: 99-27935-193 NAME/KEY: exon LOCATION: 238715..238919 OTHER INFORMATION: exon V3 NAME/KEY: exon LOCATION: 240440..240673 OTHER INFORMATION: exon W ATION: 240440..241153 SR INFORMATION: exon W2 ION: 227655..227736 INFORMATION: exon V4 NAME/KEY: exon LOCATION: 201123..201560 OTHER INFORMATION: exon S2 ION: 216836..217077 INFORMATION: exon V2 OCATION: 217671..217764 OTHER INFORMATION: exon V1 AME/KEY: exon OCATION: 246273..247802 THER INFORMATION: exon Z VAME/KEY: exon COCATION: 216836..216994 OTHER INFORMATION: exon V OCATION: 241072..241291 THER INFORMATION: exon X AME/KEY: exon OCATION: 244353..244561 THER INFORMATION: exon Y NAME/KEY: exon LOCATION: 201123..201234 OTHER INFORMATION: exon S LOCATION: 214676..214793 OTHER INFORMATION: exon T LOCATION: 215702..215746 STHER INFORMATION: exon U NAME/KEY: allele LOCATION: 168974 OTHER INFORMATION: 9 NAME/KEY: allele NAME/KEY: exon IAME/KEY: exon OCATION:

UCCATION: 17081

MANE/KEY: 311818

OTHER INFORMATION: 99-16100-147 : polymorphic base A or G
NAME/KEY: 311818

OTHER INFORMATION: 99-565-167 : polymorphic base A or G
NAME/KEY: 311818

OCCATION: 13358

OTHER INFORMATION: 99-5919-215 : polymorphic base A or G
NAME/KEY: 311818

OTHER INFORMATION: 99-24658-410 : polymorphic base A or G
NAME/KEY: 311818

OTHER INFORMATION: 99-30-3918 : polymorphic base A or G
NAME/KEY: 311818

OTHER INFORMATION: 9-300-135 : polymorphic base A or G
NAME/KEY: 311818

OTHER INFORMATION: 9-300-135 : polymorphic base A or G
NAME/KEY: 311818

OTHER INFORMATION: 9-300-133 : polymorphic base A or G
OTHER INFORMATION: 9-300-133 : polymorphic base A or G
NAME/KEY: 311818

OCCATION: 20379

OTHER INFORMATION: 9-250-128 : polymorphic base A or T
NAME/KEY: 311818

OCCATION: 20379

OTHER INFORMATION: 9-250-128 : polymorphic base A or T
NAME/KEY: 311818

OCCATION: 20379

OTHER INFORMATION: 9-250-128 : polymorphic base A or T
NAME/KEY: 311818

OCCATION: 20379

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OTHER INFORMATION: 9-250-128 : polymorphic base A or G
OTHER INFORMATION: 9-250-128 : polymorphic base A or G
OTHER INFORMATION: 9-250-128 : polymorphic base A or G
OTHER INFORMA

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General invocations:

APPLICANT: OLEK, Alexander
APPLICANT: PIEFENBROCK, Christian
APPLICANT: PIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
ITILE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2001-04-06
PRIOR PRILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-00
PRIOR FILING DATE: 2000-06-00
PRIOR FILING DATE: 2000-06-00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 AGAAATGGAGTGGCTGGAATAAAAGTGGCTGAATCATCTTCAACTCTAGTAAGATGTCAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797 AGAATATCATTTCCCCGGTCAAAATATAAGGATATTCATTAATATTATTATCAACATAC 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     917 TARATTTTGTTTTATGGACGARGTACATARTCCARGARTTTATTTTCATCTTGGAATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 CTCATTITGACCTATTITAAACAGGCCTCTTTAAATATACACTTCTCTGTAGTGTATGCT
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Pred. No. 0.054;
0; Mismatches 158; Indels
                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFREENCE/DOCKET NUMBER: NEB-131
TELEPHONE: 978-927-5054
TELEPHONE: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-204-708-6; Sequence 6, Application US/10204708; Patent No. 6677731; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2739 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence
LOCATION: 1...2736
GTHER INFORMATION:
US-08-951-871-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.2%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic DNA
          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 TTATGAGATATATCCATGTTGAATTTTGTAGCTGTGGTTTGATGATTTTTAC-ATTATAT
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   : polymorphic base G or C
                                                                                                       : polymorphic base G or T
                                                                                                                                                                                                            : polymorphic base A or C
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OPERATING SYSTEM: DOS
SOFTWARE: FRAEUSEQ Version 2.0
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/951,871
FILING DATE:
                     NAME/KEY: allele
LOCATION: 210964
OTHER INFORMATION: 8-282-260 :
NAME/KEY: allele
LOCATION: 210979
OTHER INFORMATION: 8-282-245 :
NAME/KEY: allele
LOCATION: 211050
OTHER INFORMATION: 8-282-174 :
NAME/KEY: allele
LOCATION: 21132
OTHER INFORMATION: 8-282-92 :
NAME/KEY: allele
LOCATION: 211247
OTHER INFORMATION: 8-281-367 :
NAME/KEY: allele
LOCATION: 211247
OTHER INFORMATION: 8-281-367 :
NAME/KEY: allele
LOCATION: 211315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 211366
OTHER INFORMATION: 8-281-248:
NAME/KEY: allele
LOCATION: 212520
OTHER INFORMATION: 8-279-197:
NAME/KEY: allele
LOCATION: 212821
OTHER INFORMATION: 8-278-289:
NAME/KEY: allele
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COUNTRY: US
ZIE: 0.1915
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TYPE: IBM Compatible
8-282-345
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDAL
STREET: 32 TTY: Beverly
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Gaps

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Pred. No. 0.069;
0; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                 83; Indels
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APPLICANT: Siadak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Thorne, Barbara A.
APPLICANT: Thorne, Barbara A.
APPLICANT: Barborath, Ourgen
FILE REBERENCE: DB2 SEQUENCE
CURRENT APPLICATION NUMBER: US/09/466,635
CURRENT APPLICATION NUMBER: 1999-12-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                       Score 46.2; DB 4
Pred. No. 0.069;
); Mismatches B
FILE REFERENCE: DE2a SEQUENCE
CURRENT APPLICATION NUMBER: US/09/247,352
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 09/026,291
EARLIER FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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US-08-956-171E-521/c
; Sequence 521, Application US/08956171E
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Best Local Similarity 53.6%;
Matches 96; Conservative
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                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Human and Mouse US-09-247-352-6
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Best Local Similarity
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US-09-466-635-6/c
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                                                                                                          FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                    Query Match

5.4%; Score 46.2; DB 4; Length 6669;

Best Local Similarity 29.5%; Pred. No. 0.065;

Matches 191; Conservative 0; Mismatches 456; Indels 1
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Sequence (Application US/09247352)
Patent No. 6312693
GENERAL INFORMATION:
APPLICANT: Arution (Alejandro A. APPLICANT: Barris, Linda
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A. APPLICANT: Thorne, Barbara A. APPLICANT: Huse, William D. APPLICANT: Ww. Herren
APPLICANT: Ww. Herren
APPLICANT: Watkins, Jeffry D. APPLICANT: Watkins, Jeffry D. TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
              SEQ ID NOS:
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US-09-247-352-6/c
                                                    6999
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Gaps

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GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEPENBROCK, Christian
APPLICANT: DEPENBROCK, Christian
APPLICANT: DEPENBROCK, Christian
APPLICANT: DEPENBROCK, Christian
APPLICANT: DEPENBROCK, Christian
APPLICANTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DA Assessing DNA Methylation
FILE REFERENCE: 5013.402
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: DC7/EP01/03971
PRIOR FILING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR ETLING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 20
I FRANCH AFRA
                                                                                                                                                 272 TITITATATCTICAATTTCTTTTAAGAACTCCTCACTTTGTTTTTTCAAAGTATTAAATA 213
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                  332 ATTCTAAGTCGCACTTTAATTGCTCCTCTTCATTAAAGTCTTTCAATTCAGGGTTATCTT 273
                                                                                638 TIATGITITGCTCATTTAAAAAACCTGGTTAAATATTTCACAAATCGACATTATGATAT 697
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                                                                                                                                                                                                                       212 CACTITCATATCTITCATGAGATAATCCTAGATAATCTAAATTATCAGTATTTCCATTTT
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US-10-204-708-20
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Sequence 20, Application US/10204708
Patent No. 6677731
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Best Local S
Matches 258
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                                                                                                                                                                               Craig A. Rosen
Steven C. Barash
Michael R. Fannon
INVENTION: Staphylococcus aureus Polynucleotides and Sequences
SEQUENCES: 5256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTAAAAGIGITITAATITITAACTATIATATGTCAATTTTGAACAGCTCTTTCACTTACTA 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Staphylococcus aureus P
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 521:

US-08-956-171E-521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1596
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 46,789
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                                                                                                         Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
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Best Local Similarity 26.7%;
Matches 145; Conservative
                                                                     APPLICANT: Charles
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Best Local Similarity
Patent No. 6593114
GENERAL INFORMATION:
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Search completed: August 14, 2004, 20:48:09 Job time: 85.9109 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Name	OM nucleic - nucleic search, using sw model	
US-10-082-830-99 1934cactctggctgggatgccgctagtctcgagtctag 56 table: IDENTITY NUC Gapop 10.0, Gapext 1.0 3470272 seqs, 21671516995 residues mber of hits satisfying chosen parameters: 6940544 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 DB seq length: 0 Listing first 45 summaries Genebhl:* 1: 9D ba:* 2: 9D ln:* 3: 9D ln:* 4: 9D ln:* 5: 9D ln:* 6: 9D ln:* 7: 9D ln:*	on: August 14, 2004, 07:10:17; Search (withous 9,989.84)	ime 2442.69 S alignments) Million cell
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	domo sa quence Dryza s	AL/325U3 MOUSE DNA AC135575 Rattus no AC110880 Mus muscu A1731820 Mouse DNA	iomo iomo iomo iomo iomo iomo iomo iomo	fus n fus n Moue	Rattus Mus m Mus m Mus mu	Mous Mus m Mus m Mus	AC145577 Mus muscu AC134084 Rattus no AC103213 Rattus no AC098021 Rattus no AC097127 Rattus no	Mus mu Homo E Homo E Homo E	04 Mus m 63 Rattu 420 Mous 772 Mus 58 Rattu 867 Mous	Mus Mus Ratt Ratt Ratt	linear PRI 19-MAR-1999 map 4q25, complete Vertebrata; Euteleostomi; Hominidae; Homo. D.R. and Myers, R.M.
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Best Local Similarity 1.9%; Pred. No. 0.033;
Matches 7; Conservative 218; Mismatches 141; Indels
                                                                                                                                                                                                                                                                      1 (bases 1 to 7218)
Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                             DNA
                                                                          7218 bp I
US 5670367.
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                                                                                                 14 from patent
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                                                                                                                                                                                                                                             Unclassified.
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                                                                                                 Sequence :
I66494
                                                                                                                                                  I66494.1
                                                                                                                                                                                                 Unknown
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                         RESULT 2
166494/c
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               Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.

Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.

Direct Submission

Bubmitted (23-FEB-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA (1985.66)

Stone, N.E., Schmutz, J.J., Shang, J., Cox, D.R. and Myers, R.M.

Direct Submission

E. Submitted (19-MAR-1999) Department of Genetics, Stanford Human Genome Center, 4005 Miranda Avenue, Palo Alto, CA 94304, USA On Mar 19, 1999 this sequence version replaced gi:3603082.

Gallyr: Phrap Quality >=40 100.0% of Sequence;
Estimated Total Number of Errors is 0.0.

STS Content:
SHGC-23859 G38472

WI-30731 G23237

SHGC-23843 G28477

SHGC-23843 G28477

SHGC-23843 G28477

SHGC-23843 G28477
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/clone="p159121"
Library"
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Pred. No. 6.3e-109;
0; Mismatches 1;
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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ilarity 99.6%;
Conservative
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality; as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp;, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135971 AGCCAGAAAAAATCCAGATGTCCTTCAACAGAAATGTGTACAGAAATATGGTACAT 136030
                                                                                                                                                                                                                                                                                      AL732503 148526 bp DNA linear ROD 25-JUL-2002
Mouse DNA sequence from clone RP23-2809 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 148526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clon on Jul 26, 2002 this sequence version replaced gi:21911625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-2809 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136031 TTÁCACAATGGAGTATTACTTGCCTATTAAAAAAAAATGAATTCATGAAACA 136081
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Conservative 0; Mismatches 39; Indels 0; C
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50277 MWWCCARCATAAKASYAKRRWTWW 50254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
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/clone="RP23-2809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-NOV-2003) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (04-NOV-2003) this sequence version replaced gi:24431631.

* NOTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 GGTTAAACTTATTCAAGATTGACTGAGTCTCCTATTTTCCTTAAATTTACTAGAAGTGAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 TGGCATTTAAGCATGAAGAGTAGGGCTTCTATGGTAGGGACTGGAGTAGGCAGCATTCCA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 GGAAAGGATCTCAGAGGTCAGAAACAATAGATTATCAGTTAAATACTTCTGGACCAAAGA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 AGACCTTGAAATCCTGGCTCGGTGATGTATAAATATAATACACAATGAGGTCCTT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 GAGGGTGAGTGAGTGATAGGGCTGAAGACAGGAGACAGAAGAGACAATTCAAATGTCCT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 ATACTTTTTATTTTCTTTACCTGTTACATATCAAATCTTAGGATGTATTACTTCCAAGGC 91
                                         Oryza sativa ssp. japonica cv. Nipponbare TIGR_CLONE BAC genomic
                                                                                                                                                                                                                                                                                                                          Submitted (22-OCT-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA (bases 1 to 128683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 GCTCCAAGAACTACAGAAAATAGAAGGAAAGTCTCCATTGAGCCATGAACTGTGAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 TACACAGAAGACTGATTATATAGATAATGGTACATTCATATAAACATGATATATTTACTA
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ilarity 11.9%; Pred. No. 0.14;
Conservative 232; Mismatches 208; Indels
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     Fraser, C.
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1 (Dates 1 to 94391)

RS Muzzy, D. Marie., Metzer M. Lee., Abramzon, S., Adams, C., Allder, J., Advaluano, D. Muzzy, D. Marie., Metzer M. Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Arquiano, D. Mayalebechi, V., Advagli, A., Bada, E., Badan H., Baldwain, D., Barderanaide, D., Barber, M., Barnstead, M., Benahmed, F., Brawalla, D., Barber, M., Barnstead, M., Benahmed, F., Bryan, D., Carter, C., Burrell, K., Calderon, B., Cadenas, V., Carter, C., Burrell, K., Calderon, B., Cadenas, V., Carter, M., Carter, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Dederid, D., Davis, C., Davis, C., Dederid, D., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Dederid, D., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C., Davis, C.
AC135575 94391 bp DNA linear HTG 19-OCT-2002 Rattus norvegicus clone CH230-20316, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                             Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                    GI:24137395
                                                                                                                             AC135575.1 GI:247
HTG; HTGS_PHASE1.
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                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help&bcm.tmc.edu
Contact: hgsc.help&bcm.tmc.edu
Conter: project Information
Center project name: KCOF
Center clone name: CH230-20316
Center clone name: CH230-20316
Center clone name: CH230-20316
Center clone name: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 38760 bases at least Q40
Consensus quality: 41315 bases at least Q20
Consensus quality: 42555 bases at least Q20
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1218: gap of unknown length
2501: contig of 1283 bp in length
2601: gap of unknown length
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gap of unknown length
contig of 1227 bp in length
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contig of 1135 b
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bp in length

length

gap of contig

35361:

33998

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

TITLE

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Statement B. Linton, L. Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, M., Bastien, Y., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barra, M., Bastien, Y., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barra, M., Bastien, Y., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barra, M., Bastien, A., Chango, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, B., Gord, S., Goyette, M., Gade, D., Galdgan, J., Cardyna, S., Farreira, P., FitzHugh, M., Cage, D., Galgan, J., Cardyna, S., Farreira, P., FitzHugh, M., Marquis, N., Matchews, C., McCarth, M., Mardus, P., Malfor, J., Marquis, N., Matchews, C., McCarth, M., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, P., McKernen, X., Meldrim, J., Mengan, C., McCarth, M., Spender, B., Scange-Thoman, N., Schupback, R., Sepander, B., Scange-Thoman, N., Schupback, R., Schupback, M., Viel, R., Schupback, M., Travis, N., Trigillo, J., Vessiller, B., Conderson, J., Chang, J., Marker, M., Allen, N., Anderson, S., Schupback, M., Travis, N., Trigillo, J., Vessiller, B., Conderson, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., Chang, J., 
                                                                                          AC110880 168088 bp DNA linear HTG 22-OCT-2002 Mus musculus clone RP24-456G3, WORKING DRAFT SEQUENCE, 3 ordered
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, D. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (Dases I to 16808)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-456G3
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HTG, HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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/mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 43631 83102: contig of 43630 bp in length 43631 gap of 100 bp

* 43731 83102: contig of 83972 bp in length

* 83103 168088: contig of 84886 bp in length.
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                                                   Center project inclination
Center project inclination
Center project name: 1886 G 3
Center clone name: 456 G 3
Center clone name: 456 G 3
Sequencing vertificits
Sequencing very plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167516 bases at least Q 0
Consensus quality: 167756 bases at least Q 0
Insert size: 168000; agarose-fp
Insert size: 16808; sum-of-contigs
Quality coverage: 12.3 in Q 20 bases; sum-of-contigs
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                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="RPCI-24 Male Mouse BAC"
site: http://www-seg.wi.mit.edu
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/note="assembly_fragment"
83203. .168088 --
/note="assembly_fragment"
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/note="assembly_fragment"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="RP24-456G3"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1:e., phred quality; ) an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82026 AATAGCCAGAAACTGCAAAGAATCCAGATGTCCTTCAACAGAGGAATGGATACAGAAAT 82085
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Homo sapiens clone RP11-2608, WORKING DRAFT SEQUENCE, 17 unordered
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(bases 1 to 168773)
Griffiths, C.
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from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                           Direct Submission
Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Gambridgeshire, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 29, 2002 this sequence version replaced gi:21955608.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 137648)
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8.6%; Score 48.2; DB 10;
Best Local Similarity 67.3%; Pred. No. 0.28;
Matches 68; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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AUTHORS

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418 AAGAACAGGAGACAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
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                                                 si gap of 100 bp.
3: contig of 4468 bp in length
3: gap of 100 bp.
4: contig of 6643 bp in length
4: contig of 100 bp.
5: contig of 10135 bp in length
6: gap of 100 bp.
7: contig of 10128 bp in length
7: gap of 100 bp.
8: contig of 10342 bp in length
8: gap of 100 bp.
8: contig of 26854 bp in length
9: gap of 100 bp.
9: contig of 26854 bp in length
9: contig of 26854 bp in length
9: contig of 12861 bp in length
9: gap of 100 bp.
9: contig of 12861 bp in length
9: contig of 12861 bp in length
9: contig of 12861 bp in length
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                        100 bp
of 5131 bp in length
             bp in length
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8.5%; Score 47.8; DB 2;
Best Local Similarity 61.8%; Pred. No. 0.36;
Matches 76; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5304. .7364
/note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
.5516. .20495
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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05176. 124687
note="assembly_fragment"
24788. 137648
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 137648
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="RP11-2608"
             contig
gap of
contig
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vector_side:right"
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124687:
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                                              NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 137000; agarose-fp
Insert size: 136048; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vectors: M13, M77815; 100% of reads Sequencing vectors: M13, M77815; 100% of reads Chemistry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 128694 bases at least Q40 Consensus quality: 133079 bases at least Q20 Consensus quality: 135006 bases at least Q20
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of 1813 bp in length
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of 2061 bp in length
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of 5367 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-2608
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/mol_type="genomic_DNA"
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Exercible 1. Linton L. Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S. Baldarin, J., Barna, N., Bastien, V., Bada, F., Anderson, S., Baldarin, J., Barna, N., Bastien, V., Bada, F., Cockele, A., Cackle, A., Cackle, A., Cackle, A., Cackle, A., Cackle, M., Colargelo, M., Collins, S., Collymore, A., Cackle, A., Cackle, S., Goyette, M., Burkett, G., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Carlan, L., Karatas, M., Karatas, M., Karatas, M., Karatas, M., Karatas, M., Calagan, J., Gardyna, S., Ginde, S., Goyette, M., Gardyn, M., Gardyn, M., Calagan, J., Gardyna, S., Ginde, S., Goyette, M., Machan, L., Karatas, M., Lieu, C., Iliu, G., Lamazares, R., Landares, T., Lackex, M., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPhereters, R., McGarthy, M., McEwan, P., McGurk, A., McKernan, K., McPhereters, R., McGarthy, M., Santos, S., Stonace, S., Severy, P., Spencer, B., Rothman, D., Naglatin, J., Maylor, J., McGurk, A., Santos, R., Stonace, S., Severy, P., Spencer, B., Stantas, J., Treedres, S., Severy, P., Spencer, B., Stonace, S., Severy, P., Spencer, B., Stonace, S., Schauer, S., Stonace, S., Severy, P., Spencer, B., Stonace, S., Stonace, S., Severy, P., Spencer, B., Stonace, S., Schauer, S., Lincon, L., Nubbaum, C., Lander, R., Wu, X., Wann, D., Ye, W.J., Vassilier, W., Dan, S., Mackerson, S., Barran, M., Bastien, V., Boukhgalter, B., Bircon, L., Musbaum, C., Lander, R., McKarato, B., Lincon, L., Musbaum, C., Canago, M., Carad, P., Cook, A., Cooke, P., Dearellano, K., Dawar, K., Diaz, J. S., Dodge, S., Faro, S., Ferriar, P., Dearerson, S., Barran, W., Dayan, M., Chang, J., Charace, J., Collins, S., Collimos, S., Collins, S., Cooke, P., Dearellano, K., Dawar, K., Dan, J., Stonace, J., Schauer, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Schuber, S., Sc
                                                                                                     116709 GTGGTATATTTACACACAGAAAAAAAAGGCAGTAGAAAGTTACTTCACACATCA 116650
ACO51635 158608 bp DNA linear PRI 27-AUG-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-540A4
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4 (Master L. C. 1980)

Brown, A., Camarata, J., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, P., Cook, P., Cook, P., Cook, P., Cook, A., Gord, S., Gord, S., Goyete, M., Gage, D., Galagan, J., Gazdyna, S., Ginde, S., Gord, S., Goyete, M., Gage, D., Galagan, J., Gazdyna, S., Gord, S., Goyete, M., Gardeman, T., Hame, W., Iliev, I., Johnson, R., Jones, C., Kamara, P., Kararas, A., Kells, C., LaRocque, K., Liu, G., MacLean, K., Marquis, N., Matthews, C., MacLean, P., McKernan, K., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reetra, R., Ribeack, M., Riley, R., Rise, C., Rogov, P., Steman, S., Schupback, R., Schauer, S., Schupback, Steman, S., Severy, P., Spencer, P., Steman, T., Talamas, J., Tesfaye, S., Theodore, J., Viell, R., Vole, R., Waman, D., Ye, Waman, Travis, N., Targilio, J., Yossiliev, H., Viel, R., Waman, J., Ramer, A., Milson, B., Man, M., Man, M., Man, M., Waman, D., Ye, W.J., Young, G., Mann, J., Rombers, L., Zimmer, A., and Zody, M., Young, G., Camon, J., Rommission.
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (04-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Anales Street, Cambridge, MA 02141, USA
4 (bases 1 to 158608)
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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Center clone name: 540_A_4
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Birren, B., Innton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukalater, B., Brown, A., Burkett, G., Baddalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand Flerre, N., Grand, G., Hados, B., Hadford, A., Horton, L., Howland, J.C., Iliev, I. Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakorque, K., Lamazares, R., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Maddrim, Menneus, L., Minova, T., Mirada, C., Minoya, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Oliver, J., Peterson, K., Pierre, N., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Tirgilio, J., Vassiliev, H., Wiel, R., Wu, X., Wyman, D., Ye, W.J., Young, G., Zahnoun, N., Zimmer, A. and Zody, M., Wyman, D., Ye, W.J., Simmer, A. and Zody, M., Wyman, D., Ye, W.J., Shanda, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W.J., Shanda, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W.J., Shanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda, J., Zimmer, A. and Zody, M., Sanda,
AC068678 193978 bp DNA linear HTG 31-OCT-2001
Homo sapiens chromosome 18 clone RP11-104N14 map 18, WORKING DRAFT
SOCENCE, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 1939?8) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-104N14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (06-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 28, 2001 this sequence version replaced gi:13249473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                   AC068678.3 GI:16506881
AT068678.3 GI:16506881
HTG; HTGS PHASEI; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
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Web site: http://www-seq.wi.mit.edu
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                                                                                 /clone lib="RPCI-11 Human Male BAC"
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1. 'Ypt_family="Alu8g/x"
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complement(1853. .2218)
rpt_family="L2"
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complement (3868. .4006)
rpt_family="LTR7"
011. .4167
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complement(9940. 9989)
/rpt_family="MLT11"
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957. .5984
db_xref="taxon:9606"
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                                                                clone="RP11-540A4"
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357. .3850
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731. .6769
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510. .8250
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279. .8516
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612. .8827
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487. .9805
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806. .9922
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940. .7148
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rpt_family="LIMEd"
127. .9435
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:598. .6710
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complement(4235. .4
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436. .940f
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                                                                                                                                                                                                                                                                                                                                                                         COMMENT
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Homo sapiens chromosome 18 clone RP11-153D16 map 18, WORKING DRAFT SECURICE, 40 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 193578; sun-of-chitigs
Quality coverage: 7.3 in Q20 bases; agarose-fp
Quality coverage: 7.1 in Q20 ba.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* true of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; Score 47.8; DB 2; Length 193978; 61.8%; Pred. No. 0.34; cive 0; Mismatches 47; Indels 0;
                                                                                                                                                                                59978: contig of 59978 bp in length 60078: gap of 100 bp 83937: contig of 23859 bp in length 84037: gap of 100 bp 113721: contig of 29584 bp in length 113721: gap of 100 bp 147302: contig of 33581 bp in length 147402: gap of 100 bp 19978: contig of 46576 bp in length
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1. .59978
note="assembly_fragment"
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vector_side:left"
60079. .83937
/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="18"
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HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO SADIENS (human)
HOMO SADIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="RP11-104N14"
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Best Local Similarity 61.8
Matches 76; Conservative
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Luster, B., (Dates I to 2009462).

Ritter, B., (Dates I to 2009462).

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collangelo, M., Collymore, A., Collymore, A., Collymore, P., Collymore, P., Collymore, P., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donnelan, L., Doyle, M., Ferreiza, P., Fitzhlano, K., Dewar, K., Domino, M., Donnelan, L., Doyle, M., Ferreiza, P., Fitzhlano, R., Jones, C., Fann, L., Karatas, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McTow, J., Naylor, J., Norman, C.H., O'Connor, T., Connon, P., McGurk, A., McKernan, K., McLaughlin, J., Melrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., Connon, P., Reterson, K., Pollara, V., Riley, R., Santos, R., Savery, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tarefaye, S., Tirrell, A., Vasailiev, H., Vo, A., Wheeler, J., Wu, X., Wman, D., Ye, W. J., Zimmer, A. and Zody, M.

Research, 320 Charles Street, Cambridge, Ma 20141, USA On May 25, 2000 this sequence version replaced gi: 7321509.

All repeats were identified using RepeatMasker.html

Lengal A., Fa. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases: Linton,L., Nusbaum,C. and Lander,E. Homosapiens chromosome 18, clone RP11-153D16
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Quality covers
Nors: This is a 'working draft' sequence. It currently
consists of 40 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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Contact: seguence submissions@genome.wi.mit.edu
------- Project Information
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Mus musculus chromosome 1 clone RP23-429G8 map 1, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces.
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8.5%; Score 47.8; DB 2; Length 209462;
Best Local Similarity 61.8%; Pred. No. 0.34;
Matches 76; Conservative 0; Mismatches 47; Indels 0;
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AC102621.4 GI:37633693
HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
MES MUSCULUS (house mouse)
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Inote="assembly_fragment"
5432. 27214
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7357. .8828
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21085. .23101 /note="assembly_fragment"
454. .2778
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Submitted (23-NoV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa (bases 1 to 207777)

Birreh, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Colymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard-Plerre, N., Hafez, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kanatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., Maclean, C., Mccdnald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maldrim, J., Meneus, L., Mthowa, T., Manning, V., Murphy, T., Naylor, C., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Sentus, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, J., Tavers, M., Volan, Wilson, B., Wu, X., Wanan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Mi repeats were identified a Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Mitty, A.F.A. & Green, P. (1995-1997)

http://ftp:genome.washington.edu/RM/RepeatMasker:
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Center: Whitehead Institute/ MIT Center for Genome Research
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------- Project Information
Center project name: 119119
Center clone name: 429_G-8
                                                                                                                       Birren, B., Nushaum, C. and Lander, B.
Mus musculus chromosome 1, clone RP23-429G8
Unpublished
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Web site: http://www-seq.wi.mit.edu
                                                                                              (bases 1 to 207777)
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   ORGANISM
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AUTHORS
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176220 AATAGCCAGAGACTGGAAAGAACCCAGATGTCCTTCAACAGGGGAATGGATACAGAAAAT 176161
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AC132603.2 G1:22830458
HTG, HTGS. PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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McPherson, J.D. and Waterston, R.H.
Direct. Submission
Submitted (01-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
Chaese 1 to 322906)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478 AIGGIACATICATATAAACAIGATATTTACTAATTAAAACATACCAACACACACAACA 537
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 322906)
McPherson,J.D. and Waterston,R.H.
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On Sep 13, 2002 this sequence version replaced gi:22597689.
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                        16107: contig of 16107 bp in length

16207: gap of 100 bp

87378: contig of 71171 bp in length

87478: gap of 100 bp

93646: contig of 6168 bp in length

93746: gap of 100 bp

185956: contig of 92210 bp in length

186055: gap of 100 bp

207777: contig of 21721 bp in length
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/clone_lib="RPCI-23 Female Mouse BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="1"
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Best Local Similarity 61.1%;
Matches 77; Conservative (
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* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as 'runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                   Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Sequencing vector: M15, 0%
Chemistry: Dye-terminator B19 Dye; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 315826 bases at least Q30
Consensus quality: 317973 bases at least Q20
Insert size: 223000; agarose-fp
Insert size: 322006; sum-of-contigs
Quality coverage: 13.22 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 14860 bp in length contig of unknown length contig of 36455 bp in length gap of unknown length contig of 93882 bp in length contig of 93882 bp in length contig of 162600 bp in length gap of unknown length gap of unknown length contig of 16260 bp in length contig of 1237 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1483: contig of 1483 bp in length 1583: gap of unknown length 3419: gap of unknown length 3419: gap of unknown length 4847: contig of 1428 bp in length 4947: gap of unknown length 8951: contig of 4004 bp in length 9051: gap of unknown length 13372: contig of 4321 bp in length 13472: gap of unknown length
                    Contact: submissions@watson.wustl_edu
------- Project Information -------
site:http://genome.wustl.edu/gsc/index.shtml
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note="assembly_name:Contig12"
420. .4847
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note="assembly_name:Contig13"
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3473. .28332
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note="assembly_name:Contig18"
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58970. .321569
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21670. .322906
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note="assembly_name:Contig15"
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db_xref="taxon:10090"

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                                                              Center project name: M_BB0066C10
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a Yac.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL: Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at the continuous and regions are used to associate primary and the continuous manager. Accound at the continuous manager ac.uk/Projects/C elegans/wormpep RP24-173B15 is from a Male (CFSPL/64) mouse BAC Library VECTOR: pTARBACI.
                                                                                                                                                                                      23449 AATAGCAAGAAGCTGGAAAGAACCCAGATGTCCCTCAACAGAGGAATGGATACAGAAAAT 23390
                                                                                                                                                                                                                                                                                                23389 AIGGIICATITACACAAIGGAGAACIACICAGCIAITAAAACCAAIGAACICACAAAAIT 23330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX537253 161021 bp DNA linear ROD 04-OCT-2003 Mouse DNA sequence from clone RP24-173B15 on chromosome 2, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-007-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquery@sanger.ac.uk Clone requests. clonerequest@sanger.ac.uk
not 5, 2003 this sequence version replaced gi:32812728.
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
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                                                                                                                          418 AAGAACAGGAGACAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                  478 ATGGTACATICATATAAACATGATATATITACTAATTAAAACATACCAACACACACAACA
Length 322906;
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0
                                                                  49; Indels
   Score 47.6; DB 2;
Pred. No. 0.35;
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                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/db_xref="taxon:10090"
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BX537253.6 GI:37518523
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Humphries, M.
8.5%;
                                                           77; Conservative
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                             Similarity
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   Query Match
Best Local &
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BX537253/c
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Muzny, D. Marte., Metaker, M. Lee., Abramzon, S., Adams, C., Alder, J., Albancoks, S., Amin, A., Anguiano, D., Allen, T., Alsbrooks, S., Amin, A., Anguiano, D., Allen, T., Anguiano, D., Angalebechi, V., Angadi, A., Apodeji, M., Baca, E., Baden, H., Blaik, D., Blaik, D., Barber, M., Barnstead, M., Bearle, B., Brawh, D., Blaik, D., Blaik, D., Barber, M., Barnstead, M., Blaik, D., Blaik, D., Blaik, D., Blaik, D., Blaik, D., Chen, G., Chavazo, T., Chavazo, T., Chavazo, D., Chen, G., Chavazo, D., Chen, G., Chen, G., Chen, T., Chen, G., Chen, M., Cree, A., D'Souza, D., Davolla, M. D., Denson, S., Deramo, C., Digg, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Deramo, C., Digg, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Deramo, C., Digg, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Fugene, C., Evans, C.A., Falls, T., Rayes, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Gebra, M., Hanlton, K., Hanlton, K., Hanlton, K., Hanlad, M., Hanll, C., Hamilton, C., Hamilton, K., Hanlton, K., Hanlad, M., Hanll, C., Hamilton, C., Hamilton, K., Johnson, R., Jacob, L., Jang, H., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Mark, M., Martin, M., Mahloy, M., Martin, M., Mahloy, M., Martin, M., Mahloy, M., Martin, M., Mahloy, M., Martin, M., Mandarthe, M., Martin, M., Mantin, M., Mann, M., Martin, M., Mann, M., Martin, M., Mann, M., Martin, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., Mann, M., 
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                                                                                                                                                                                                                                                                                                                                                         AC133842 220394 bp DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-185E3, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                             356 ATGIATACATATITAATACACAATGAGAAGCTCCTTGAGGGTGAGTGAGTGATAGGGC 415
                                                                                                                                                                                                                                                                                                                                                                                                                              416 TGAAGAACAGGACAGAAGACAATTCAAATGTCCTTACACAGAGACTGATTATAGA 475
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476 TAATGGTACATTCATATAAACATGATATTTACTAATTAAAACATACCAACACACA
                                                                                                                                                            Length 161021;
                                                                                                                                                                1 8.4%; Score 47.4; DB 10; Length 1 ilarity 54.2%; Pred. No. 0.43; Conservative 0; Mismatches 81; Indels
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Rattus norvegicus (Norway rat)
/chromosome="2"
/clone="RP24-173B15"
/clone_lib="RPCI-24"
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                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                  96;
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AC133842
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* i 220394: contig of 220394 bp in length.
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodegren, E., Song, X.-Z., Sorelle, R., Sosa, J., Strong, R., Sutton, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, A., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, G., Warren, B., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Genome Sequencing Consortium.

Direct Submission

Submitted (19-SBP-2002) Human Genome Sequencing Center, Department Genelular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 220394)

Rat Genome Sequencing Consortium.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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/db_xref="taxon:10116"
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/clone="CH230-185E3"
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2 (bases 1 to 220394)
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8.3%; Score 47; DB 2; Length 220394;
Best Local Similarity 64.0%; Pred. No. 0.51;
Matches 71; Conservative 0; Mismatches 40; Indels 0;
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site:EcoRl
complement (219195. .219782)
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site:EcoRl
end.sequence:BH263108"
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LIGT-GSS-dog-17000359973606 Dog Library Canis familiaris genomic,
genomic survey sequence.
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22875432
14512627
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknesetigr.org
AQ933978 RPCI-23-4
ALC096539 ALE5369
ALE53699 ALE5369
ALC09659 ALE5369
ALC09659 ALE531A
AC10170 RPCI-23-4
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Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 679)
Kixness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
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BZ1001350

BX097137

BX0911359

BH069264

BH0692643

BH068169

BH088169

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BX346426

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BX346426

BX3464360

AZ367086

AZ367086
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AZ278295
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AZ375839
AQ923677
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BE635285 uv60a02.y
AZ003793 RPCI-23-3
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                                                                                                 August 14, 2004, 07:10:17; Search time 1929.83 Seconds (without alignments) 8711.839 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB
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Length 535;

Indels

GSS 24-FEB-2000

linear

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamwalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (baees 1 to 444)

2B 1 (baees 1 to 444)

2B 2 hao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

4L Unpublished (1999)

4L Unpublished (1999)

5Cher GSS: RPCI-23-345A18.TUB

6Chard GSS: RPCI-23-345A18.TUB

6Chard GSS: RPCI-23-345A18.TUB

7L Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

7el: 301 838 0200

7ex: 301 838 0200

7ex: 301 838 0200

8mail: Salao@rigir.org

7el: 301 838 0200

8mail: Salao@rigir.org

7el: 302 are derived from the mouse BAC library RPCI-23. For BAC

7el: 302 are derived from the mouse BAC library RPCI-23. For BAC

7el: 302 are derived from the mouse BAC library RPCI-23. For BAC

7el: 302 are derived from the mouse BAC library RPCI-23. For BAC

8mail: Salao@rigir.org

7el: 302 are derived from the mouse BAC library RPCI-23. For BAC

8mail: Salao@rigir.org

8mail: Salao@rigir.org

8mail: Salao@rigir.org

8mail: Group availability, please contact Pieter de Jong

7el: Arow: A column: 18

8cq primer: 77

6lass: BAC ends

7el: Arow: A column: 18

8cq primer: 77

6lass: BAC ends

7el: Arow: A column: 18
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//lab host="Dt108"
/clore lib="Rpt02"
/clore lib="Rpt02"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector lib organization of brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH108 electrocompetent cells (BRL Life Technologies). "
                                                                                                         418 AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
                                                                                                                                                                                                      150 AATAGCCAGAAGCTGGAAAGAACCCAGATGTCCCTCAACAGAGGAATGGATACAGAAAAT 91
                                                                                                                                                                                                                                              90 Argeracartraracaargrieracracrecerarraaaaccaacaarrracaaarr 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPCI-23-345A18.TV RPCI-23 Mus musculus genomic clone RPCI-23-345A18, genomic survey sequence.
       8.6%; Score 48.2; DB 10;
11.6%; Pred. No. 0.39;
ve 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol type="genomic DNA"
'strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ003793.1 GI:7079149
                                        61.6%;
                                                            77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                     Similarity
                                                                                                                                                                                                                                                                                                   538 CCTCG 542
                                                                                                                                                                                                                                                                                                                                              CTTAG 26
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               Query Match
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Matches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ003793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (basea 1 to 535)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                         429 ACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGGTACATTC
                                                                                                                                                                                                                                                                                                                               Gaps
                                                    /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                            8.6%; Score 48.4; DB 29; Length 679; 68.4%; Pred. No. 0.34; tive 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 ATATAAACATGATATATTAACTAATTAAAACATACCAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 ATATAAGAAACACTATACAATGATGAAAATCAACAAA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40RP from Gibco
High quality sequence stop: 482.
Localion/Qualifiers
Localism="Mus musculus"
/mol type="maRA"
/strain="CS7BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
clone="IMAGE:3411530"
                 Location/Qualifiers
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Mus musculus
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                                                                                                                                                                                                                                                                                                           Similarity 68.4 57; Conservative
Class: shotgun.
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Best Local S
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                    FEATURES
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8.4%; Score 47.4; DB 28; Length 444;

В à Dp

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Contact: Shaying Inactions
Contact: Shaying Inactions
Contact: Shaying Inactions
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: schaodigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter dejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/fdb/bac_ends/mouse/bac_end_intro.html
Plate: 286 row: P column: 18
Seq primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSS: RPCI-23-286P18.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Pemale"
/lab host="PH10B"
/clone_lib="RPCI-23"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain, Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Pemale C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                   418 AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
                                                                                                                                                                                                                                   300 AATAGCAAGAAGCTGAAAACAACCCAGATGTCCCTTAACAGAAGAATTGATACAGAAATC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
1 (bases 1 to 666)
                                                                                                                                   Gaps
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                                                                                   Length 459;
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RPCI-23-286P18.TV RPCI-23 Mus musculus genomic clone
RPCI-23-286P18, genomic survey sequence.
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                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
        and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                    360 Arggracartracacaargaagracrarrcagcrarraaaa 400
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                                                                                   28;
                                                                                Score 46.6; DB Pred. No. 0.95; 0; Mismatches
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/strain="C57BL/6J"
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/clone="RPCI-23-286P18"
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66.3%;
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                                                                                                                                                                                                                                                                                                                                                      AZ620342 459 bp DNA linear GSS 13-DEC-2000 1M0453J01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0453J01 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
Contvarsity of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 184112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLI0-Gold, T1-resistant, F-"/clone_lib=mouse_lokb plasmid UGGCM library."
/note="Wector: PWD4Znv, Purified genomic DNA from musculus C57BL/6J (male) was obtained from the Jackson
                                                                          427 AGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGGTACAT
                                                                                                                        327 AGCCAGAAAAAATCCAGATGTCCTTCAACAGAGGAATGTGTACAGAAATATGGTACAT
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                             41; Indels
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Insert Length: 10000 Std Error: 0.00
Plate: 0453 row: J column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 459.
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/strain="C57BL/6J"
  Pred. No.
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/clone="UUGC1M0453J01"
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Mus musculus
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  63.78;
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                             Conservative
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Fax: 801 585 7177
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CNS0106X 1101 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
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AL553699 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI080YE16 5-PRIME, mRNA sequence.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1201)

1 (J. W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12893776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: Seqrefégenoscope.ons.fr. Web : www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2105.r
Contact: Feng Liang Email: filiang@lifetech.com URL:
http://fulllength.livvitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO80BCO8QPI.
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/db_xref="taxon:9606"
/clone="CS0DI080YE16"
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69;
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Other GSSs: RPCI-23-429Gs.TJ

Contact: Shaying Zabo

Contact: Shaying Zabo

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library RPCI-23. For BAC

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 429 row: G column: 8
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/lab host="DH109"
/lab host="DH109"
/loote="Th109"
/note="Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Grgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Grgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Grgan: Kidney/Brain; Vector: pBACe3.6 or Site_1:
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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RPCI-23-429G8.TV RPCI-23 Mus musculus genomic clone RPCI-23-429GB,
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mogann,S., Tsegaye,G., Geer,K., Krol,M., de Mouse BAC End Sequences from Library RPCI-23
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                                                                              258 AATAGCCAGAAGCTGAAAAAAAACCCAGATGTCCCTCAACAGAAGAAGAATGGTTACAGAAAT 317
                                        AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
                                                                                                                                      318 GIGGIACATITATACAAIGGAGCACTACICAGCTATIAAAAAIGATAAATTCACGAAATI 377
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ilarity 62.8%; Pred. No. 1.4;
Conservative 0; Mismatches 42; Indels
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/organism="Mus musculus"
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strain="C57BL/6J"
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'clone="RPCI-23-429G8"
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-38618
Fax: (206) 616-38618
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availablity, please contact Pieter de Jong
(pieter@dejong.med.bhffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web_Server:
Plate: 907 row: M column: 15
Seg primer: SP6
Class: BAC ends
High quality sequence stop: 456.
                                                                                                                 AQS56776 110ear GSS 29-MAY-1999 HS_5331_A1_G08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=907 Col=15 Row=M, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                        Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Glome "lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 456)

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                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapp scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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           1058 AKAKADDKDKDAKKDDADKAKKAKAKDAKAKAKAKAK 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=907 Col=15 Row=M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 28;
Pred. No. 2.3;
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                                                                                                                                                                                                      AQ556776.1 GI:4916508
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                                                                                                                                                                                                                                                 (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 75; Conservative
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                                                                                                                                                                                                                                                 Homo sapiens
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                                                                        RESULT 9
AQ556776
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                                                                                                                                                                                                                                                   Direct Submission
Submitted (123-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.)
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melangqaster BAC library (Dros BAC) was made by Alain Billaud at CEFH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     тккитстстнитттититититититеттсттотититититетти 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTGAGGCTCCAAGAACTACAGAAAATAGAAGGAAAGTCTCCATTGAGCCATGAACTGTG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 AGCACCTGGCATTTAAGCATGAAGAGTAGGGCTTCTATGGTAGGGACTGGAGTAGGCAGC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 ATTCCAGGAAAGGATCTCAGAGGTCAGAAACAATAGATTATCAGTTAAATACTTCTGGAC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGAAGACCTTGAAATCCTGGCTCGGTGATGTATACATATTTAATACACAATGAGAAG 385
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    from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               386 CICCTIGAGGGTGAGTGAGTGATAGGGCTGAAGACAGGAGACAGAAGACAATTCAAA
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                                                                                                                        Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/mol_type="genomic DNA"

/db_xref="taxon:727"

/clone="BACN03K20"

/clone lib="DrosBAC"

/plasmid="pBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 TTACTAATTAAAACATACCAACACACACACACCTCGAG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 29;
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                                                                                                           (fruit fly)
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Pred. No. 1.
                         fly), genomic survey sequence.
AL098595
BACN03K20 of DrosBAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                        melanogaster
                                                               AL098595.1 GI:5610206
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Best Local Similarity
Matches 99; Conserv
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TITLE
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BX097137/c
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/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). "
                                             GSS 09-MAY-2000
                                                                                                                                                                                                                                                             1 (bases 1 to 539)
Zhao, S., Niernan, W., Feldblyum, T., Malek, J., Shatsman, S.,
Zhao, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhaogtigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
ACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACGATTATAGATA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 AATAGCCAGAAGCTGGAAAGAACCCAGATGTCCCTCAACAGAGGAATGGATACAAAAAT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 AIGGIACATICATATAAACAIGATATITACTAATTAAAACATACCAACACACACACA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                RPCI-23-452H21.TV RPCI-23 Mus musculus genomic clone RPCI-23-452H21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 45; DB 28; Length 539;
60.0%; Pred. No. 2.2;
live 0; Mismatches 50; Indels
                                             linear
                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: RPCI-23-452H21.TJ
Concact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Ganomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism≈"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-452H21"
                                             239 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                 AZ101750.1 GI:7754806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                    Mus musculus
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Matches 75; Conserv
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                                                                DEFINITION
RESULT 10
AZ101750
                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                      KEYWORDS
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RESULT 11 BZ160642

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Email: szzacetigr.org
chones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAND/113/
BX097137 Soares multiple sclerosis ZNbHMSP Homo sapiens cDNA clone
BX697137 IMAGE:280131, mRNA sequence.
             GSS 11-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
BZ160642
CH230-327L4.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-327L4, genomic survey sequence.
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                Loads, Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSS: CH230-327L4.TJ
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
PATZ Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 327 row: L column: 4 Seq primer: T7 Class: BAC ends.
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/clone lib="GRORI-230 Segment 2"
/none="Vector: pTARBAC1.3; Site 1: Mbo1; Site 2: Mbo1;
CHORI-230 Rat (BN/SsNHsd/MCW) BĀC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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65.3%; Pred. No. 2.2;
tive 0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"/strain="BN/SSNHsd/MCW"
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/clone="CH230-327L4"
                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                         BZ160642.1 GI:23801598
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BX097137.1 GI:27843097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 784)
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KEYWORDS
SOURCE
ORGANISM
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Location/Qualifiers
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Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pieter de Jong"
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AK081359.1 GI:26099867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Female"
                         (bases 1 to 897)
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les 66; Conserv
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGP98104619.

RZPD; IMAGP98104619.

RZPDIIIS; I.M.A.G.E. CDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDIIB NO.972)

http://www.rzpd.de/CloneCards/cgi-bin/showiib.pl.cgi/response7libNo-972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 111

Fax: +49 30 32639 111

www.rzpd.de
This clone is available royalty-free from RZPD; Contact RZPD; Contact RZPD (cloneGrzpd.de) for further information. Seg primer: Location/Qualifiers
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae,
                                  Neubert, P.; Partsch, E., Peters, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ178903 BY bp DNA linear GSS 11-OCT-CH230-443P16.TJB CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-443P16, genomic survey sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998N04619 ; IMAGE:280131"
             1 (bases 1 to 794)
Ebert, L., Heil, O., Hennig, S., Neuber Radelof, U., Schneider, D. and Korn, B. Human Unigeneset - RZPD3
Contact: Ina Rolfs
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Pred. No. 2.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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Matches 6
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                                                          TITLE
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BZ178903
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Rhygs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSS: CH230-443P16.TV
Contact: Shaying Zhao Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: Schao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Uong (Gdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 443 row: P column: 16
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: Mbo1; Site_2: Mbo1;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
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65.3%; Pred. No. 2.1;
ive 0; Mismatches 35; Indels
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High-efficiency full-length cDNA cloning
weth. Enzymol. 303, 19-44 (1999)
99270253
10349636
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-443P16"
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Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
9712 Medical Center Dr., Rockville, MD 20850, USA
1e1: 301 838 0200
Fax: 301 838 0200
Email: szhao@igr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Refere de Jone
(apdejong@mail.cho.org). Clones may be purchased from BACPAC
(Redojong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 257 row: C column: 9
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                 2369 ATGGTACATTACACAATGGTATACTACTCAGCAATTAAAAACAATGAATTCATGAATT 2428
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RPCI-24-257C9.IJ RPCI-24 Mus musculus genomic clone RPCI-24-257C9,
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Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegayo,G., Gerr,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical HMG-I and HMG-Y DNA-binding domain (A+T-hook) containing protein (InterPro|IPR00637, evidence: InterPro)"
                                                                                                                                                                                                                                                     418 AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA
                                                                                                                                                                                                                                                                                                      Length 3211;
                                                                                                                                                                                                    50; Indels
                                                                                                                                          Score 45; DB 11;
Pred. No. 1.8;
0; Mismatches 50;
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/strain="C57BL/6J"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Adachi, 770 full-length CDNAs

E (bases 1 to 3211)

RS Adachi, 7. Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furnoo, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furnoo, M., Hanagaki, T., Hara, A., Hashizume, W., Ratoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kolima, Y., Kondo, S., Konno, H., Kowai, J., Nakusi, C., Ratsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shibata, K., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Sanoh, H., Sakai, F., Takaku-Akahira, Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Direct Submission Hayashizaki, Y. Direct Submission Hayashizaki, Y. Direct Submission Hayashizaki, Y. Direct Submission Hayashizaki, Y. Direct Submission Institute, 1-7-2 Subhiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegescriken.go.jp,, URL:http://genome-gescriken.go.jp,, Tel:81-45-503-922, URL:http://genome-gescriken.go.jp,, Tel:81-45-503-922, URL:http://genome-gescriken.go.jp,, Tel:81-45-503-922, URL:http://genome-gescriken.go.jp,, Tel:81-45-503-922, URL:http://genome-gescriken.go.jp,, Tel:81-45-503-922,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase II Team and the
                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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/mol type="mRNA"
/strain="C57BL/6J"
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/coll type="Spleen/Brain"
/clone lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
/RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
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Nucleotid Human imm

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Human Human

Sequence:

Run on:

Searched:

Database

Result No. 22220997432210999746

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The invention relates to breast specific nucleic acids (BSNA) and breast-specific polypeptides (BSP). Also included are a method for determining the BSNA in a sample, a vector comprising a BSNA, a host call comprising the vector, a method for producing a polypeptide encoded by a BSNA, an anti-BSP antibody and a method for determining the presence of a BSP in a sample. The breast-specific nucleic acids, polypeptides and compositions comprising them are useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer, mammary tumour and non-cancerous disease states in breast tissue, for identifying breast tissue, for monitoring, identifying and/or designing agonists and antagonists of the polypeptides; in gene therapy; in producing transgenic animals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, ss, breast specific nucleic acid, BSNA, breast cancer, mammary tumour, cytostatic, gene therapy, non-cancerous breast disorder.
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AAF304664
AAL07097
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WO200236807-A2.
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breast cancer
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             GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                       nucleic search, using sw model
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ABA08211
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ADC87619
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                                                                                                                                                                                                                                                                                                                      120
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            and as elements in an array or computer program for pattern recognition of breast disorders. The nucleic acids may be used as hybridisation probes to detect, characterise and quantify hybridising nucleic acids in, and isolate hybridising nucleic acids from, both genomic and transcript-derived nucleic acid samples. The BSP protein may be used in a vaccine composition for raising an immune response against breast cancer. The present sequence is BSNA cDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ss; transgenic; drug metabolism; behaviour; PCR; primer; mouse; pharmacokinetic assay; pharmacodynamic assay; toxicology; serum albumin; alpha-acidic glycoprotein; CYP; multidrug resistance protein; MRP; uridine diphosphoglucuronosyl transferase; UGT; cytochrome P450.
cells, for producing engineered breast tissue for treatment and research;
                                                                                                                                                                                                                                60
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                                                                                                                                                                Length 563;
                                                                                                                                     Sequence 563 BP; 191 A; 99 C; 118 G; 155 T; 0 U; 0 Other;
                                                                                                                                                                                               0; Indels
                                                                                                                                                                tch 100.0%; Score 563; DB 6; I sal Similarity 100.0%; Pred. No. 6.1e-141; 563; Conservative 0; Mismatches 0;
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This invention relates to a transgenic non-human animal which may be used for assessing the behaviour and/or metabolism of a drug in another animal and/or metabolism. The invention also comprises a nucleic acid construct of and which expresses a foreign polypeptide associated with drug behaviour and/or metabolism. The invention also comprises a nucleic acid construct for use in producing the metabolism and/or behavior of a drug in an animal and a method of interest, comprising administering a test agent to the transgenic animal and conducting analytical tests to determine drug metabolism and/or behaviour. The transgenic animal is useful in studying drug metabolism and/or behaviour in other animals. The nucleic acid construct is useful in producing, breeding and using transgenic animal and the methods are used for producing, breeding and using transgenic animals for pharmacological studies. Nucleic acid sequences used within the invention are serum attuding allowed and using gransgenic animal and the invention are serum cliphosphoglucuronosyl transferase (UGT); multidrug resistance proteins and (MRP's). The present sequence represents a PCR primer used to create
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
                                                                                                                                                                                                                                                         New transgenic non-human animal expressing a foreign polypeptide associated with drug behavior and/or metabolism, useful for studying the behavior and/or metabolism of a drug in other animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 ATGGTACATTCATATAAACATGATATATTTACTAATTAAAACATACCAACACACAACA
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                                                                                                            2001AU-00004467.
                                                                      2002WO-AU000485.
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02.MAR.2000; 2000US-0186350P.

16-MAR.2000; 2000US-0189874P.

17-MAR.2000; 2000US-0199874P.

18-AR.2000; 2000US-0198123P.

19-MAY.2000; 2000US-0205515P.

07-JUN-2000; 2000US-021486P.

28-JUN-2000; 2000US-021486P.

30-JUN-2000; 2000US-0216647P.

07-JUL-2000; 2000US-0216647P.

07-JUL-2000; 2000US-0216647P.
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2000US-0218290P.
2000US-0220963P.
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   The invention relates to human polymucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to prytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polympoptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                  Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 CAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATAGATAATGGTACATTCA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 7.5%; Score 42.4; DB 4; Length 445; Local Similarity 62.0%; Pred. No. 0.22; es 67; Conservative 0; Mismatches 41; Indels (
                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 7935; 1399pp + Sequence Listing; English.
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                                                                                                                                                        Tang YT, Liu C, Drmanac RT;
                                                                      26-FEB-2001; 2001WO-US004927
                                                                                             28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
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                                                                                                                                                                               WPI; 2001-514838/56.
                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                            P-PSDB; AAC07944.
                        WO200164835-A2
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Homo sapiens
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                                               07-SEP-2001
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Gaps

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1006.
                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                               387 TCCTTGAGGGTGAGTGAGAGTGATAGGGCTGAAGAACAGGAGAGACAAAGACAAAT
                                                                                                                                                                                                                                                                                                                                      447 GTCCTTACACAGAAGACTGATTATAGATAATGGTACATTCATATAAACATGATATATT
Disclosure; SEQ ID NO 10207; 1297pp + Sequence Listing; English
                                                                                                                                                  Sequence 7374 BP; 1974 A; 1512 C; 1461 G; 2427 T; 0 U; 0 Other;
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ID ABA08211 standard; DNA; 7374 BP.
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   X \times S S S S S S S X S S S X S S S S X S S S X S S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X S X 
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HUMAN GENOME SCI INC (HUMA-)

Barash SC, Ruben Rosen CA,

WPI; 2001-488786/53.

New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer.

Disclosure; SEQ ID NO 1006; 577pp + Sequence Listing; English.

The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB1043-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, or ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, or breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, and and ulcerative colitis; (c) cantiovascular disorders e.g. erebral anoxia and epilepsy; and (f) cardiovascular disorders e.g. erebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly XX

Sequence 7374 BP; 1974 A; 1512 C; 1461 G; 2427 T; 0 U; 0 Other;

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Mismatches

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ADC87620/c
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                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid retwaemia, Alzhahmer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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0
                                                                                                                446
                                                                                                                                                                                                    506
                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, immune system disease, cytosine methylation, antiasthmatic, antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective, anti-HIV; anticonvulsant, ophinalmological, antirrhritic, antidiabetic, antipsoriatic, antimatematic; antimatematics, antianabetic, antipsoriatic, antiminatematicy, cancer, eye disease, arteriosclerosis, anaemia, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis, bowel disease; gene;
                                                                                                                TCCTTGAGGGTGAGTGAGTGATAGGGCTGAAGAACAGGAGAGACAAGTTCAAAT
                                                                                                                                                                                                    GTCCTTACACAGAAGACTGATTATATAGATAATGGTACATTCATATAAACATGATATAT
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16766 BP; 4604 A; 267 C; 3632 G; 8263 T; 0 U; 0 Other;
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                         Length 7374;
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                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 2130.
                                                                      26;
                              4
                            Score 42.4; DB
Pred. No. 0.53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL34157 standard; DNA; 16766
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2000DE-01043826
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                                7.5%;
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                                                                                                                                                                                                                                                                                               507 TACTAATTAAAA 518
                                                                                                                                                                                                                                                                                                                                         971 CAGCAATAAAA 960
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
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         Query Match
Best Local Similarity
...a 76; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17.
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
ABL3415/C
ID ABL3415
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DT 26-MAR.
DE Human;
XW Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel polynucleotide encoding a guanosine triphosphare-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphare-binding protein coupled receptor. The protein sequences shown in ADC87618-ADC87623 represent polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485
481
                                                 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; human; GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 144792 BP; 39827 A; 32142 C; 33413 G; 39310 T; 0 U; 100 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 GAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 ACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATAGATAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                           ;
0
                                                                                               Length 144792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NASAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                     Human GPCR related polynucleotide SEQ ID NO:2073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9667 TGCATCTATTCATGAGATATTTAGATTTA 9638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.7;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, SEQ ID NO 2073; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
Pred. No. 1
                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                       620/c
ADC87620 standard; DNA; 144792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002EP-00013517.
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ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-2001; 2001JP-00246789.
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-315783/31.
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy
                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004
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RESULT 8 ADC87619/c

DB 6; Length 16766;

7.5%; Score 42; DB 6 60.5%; Pred. No. 0.88;

Query Match Best Local Similarity

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triphosphate-binding protein coupled receptor (GPCR). A polymucleotide of the invention may have a use in gene therapy. The polymucleotide and polymeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the quanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADCR7618-ADCR7623 represent polymucleotide sequences related to the invention.
                                                                                  ds; human; GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 GAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGGTACA 485
                                                                                                                                                                                                                                                                                             New polynuclectide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 349981 BP; 100900 A; 78560 C; 77396 G; 92823 T; 0 U; 302 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                              invention relates to a novel polynucleotide encoding a guanosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 42; DB 9; Length 349981; 66.7%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stomach cancer related gene sequence SEQ ID NO:2740.
                                                                                                                                                                                                                       (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                             Human GPCR related polynucleotide SEQ ID NO:2072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309668 IGCATCIATTCATGAGATATTTAGATTTA 309639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICATATAAACATGATATATTTACTAATTA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                      Suwa M, Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 2072; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL64403 standard; DNA; 167343 BP
ADC87619 standard; DNA; 349981 BP
                                                                                                                                                                                                   18-JUN-2001; 2001JP-00246789.
                                                                                                                                                                              18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                         01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                          WPI; 2003-315783/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                             gene therapy.
                                                                                                                 Homo sapiens
                                                                                                                                      EP1270724-A2.
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                    ADC87619;
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The present invention describes a method (MI) for screening for an anti-
neoplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 847 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in
expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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03-OCT-2000; 2000US-0237606P
03-OCT-2000; 2000US-023760P
01-NOV-2000; 2000US-023760P
01-NOV-2000; 2000US-0244867P
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25-SEP-2000; 2000US-0235280P.
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2000US-0235711P.
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25-SEP-2000; 2000US-0235077P.
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02-OCT-2000; 2000US-0237173P
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                                                                                                                                     30-MAY-2001; 2001WO-US010838
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WO200194629-A2.
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159637 ATTGTTCAAAATAACAAAAGATTGGAAAGAAGGCAAATATCCTTGAGTAGAAGACTGATG 159696
the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                         409 ATAGGGCTGAAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid,
stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous,
cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                                                                                    Sequence 167343 BP; 49550 A; 37098 C; 35753 G; 44929 T; 0 U; 13 Other;
                                                                                                                                                                                                Gaps
                                                                                                                                                            Score 41.2; DB 6; Length 167343; Pred. No. 3;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thyroid cancer related gene sequence SEQ ID NO:5576.
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                                                                                                                                                                             1 Similarity 67.4%;
58; Conservative
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28-SEP-2000; 2000US-0236109P.
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Best Local Similarity
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                                                                                                           tumour
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The present invention describes a method (M1) for screening for an anti-
neoplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
to ABL70110), or is at least 95% identical to (S), where a change in
expression is indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening an
anti-neoplastic agent, and can be used for producing a product which is
the data collected with respect to the anti-neoplastic agent as a result
of M1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
prostate or pencreatic cancer, adenocarinoma, carrioma, class cell
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159637 ATTGTTCAAAATAACAAAAGATTGGAAAGAAGGCAAATATCCTTGAGTAGAAGACTGATG 159696
                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 167343 BP; 49550 A; 37098 C; 35753 G; 44929 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 ATAGGGCTGAAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATT
                                                                                                                                                                                                                                                                                                                                             Carter KC, Ebner R, Endress G, Horrigan S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 5576; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK83502 standard; cDNA; 77425 BP.
                                 2000US-0236891P.
                                                                      2000US-0237173P.
                                                                                     2000US-0237278P.
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                                                                                                                                                                                                                                                                                                          (AVAL-) AVALON PHARM.
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                                                  02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
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03-OCT-2000;
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Soppet DR,
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ABK83502/c
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39110 GCATAGCCTCAAACTAGAAACAATCCAAATGTCCACTAAGAGCAGAGCTAACAATAAAT 39051

39050 GGTGGTATATTCATATATCCTTATATTCTATGGAATATAACAATGAGAATGCATA 38995

417 GAAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGAT 476

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ftp.wipo.int/pub/published_pct_sequences
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK84885 standard; DNA; 17032 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fundal infection; sterile inflammatory disease, psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; acrdiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease, crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 73; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2001; 2001WO-US030821.
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2000US-0184664P.
2000US-0186350P.
2000US-0189874P.
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                                                                       Homo sapiens.
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17-MAR-2000;
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7.2%; Score 40.8; DB 6; Length 77425;
Best Local Similarity 59.5%; Pred. No. 3;
Matches 69; Conservative 0; Mismatches 47; Indels 0;
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PR 06-SEP-2000; 2000US-02314419.

PR 08-SEP-2000; 2000US-02314419.

PR 08-SEP-2000; 2000US-02314419.

PR 08-SEP-2000; 2000US-02314419.

PR 08-SEP-2000; 2000US-02319168.

PR 14-SEP-2000; 2000US-02319168.

PR 14-SEP-2000; 2000US-023299.

PR 14-SEP-2000; 2000US-023299.

PR 14-SEP-2000; 2000US-023299.

PR 14-SEP-2000; 2000US-023299.

PR 14-SEP-2000; 2000US-023299.

PR 14-SEP-2000; 2000US-023299.

PR 14-SEP-2000; 2000US-023399.

PR 14-SEP-2000; 2000US-023399.

PR 14-SEP-2000; 2000US-023399.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

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PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023499.

PR 25-SEP-2000; 2000US-023469.

PR 25-SEP-2000; 2000US-023469.

PR 25-SEP-2000; 2000US-0244417.

PR 25-SEP-2000; 2000US-0244417.

PR 26-CCT-2000; 2000US-0244417.

PR 26-CCT-2000; 2000US-0244617.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246418.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246528.

PR 26-CCT-2000; 2000US-0246
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I)
anino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polyvariclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
expression by rectifying mutations or deletions in aptient's genome
complement the patients own production of (I). Additionally, (I)
that affect the activity of (I) by expressing inactive proteins or to
cupplement the patients own production of (I). Additionally, (I)
coupling and a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
concers and cancer menune/haematopoietic-related diseases, especially
cancers and cancer mecastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
concers and cancer mecastases of haematopoietic antigen genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 ATTATGCTTAACAGCCCCAAACTGGAAATAATTCAAATGTCCATTAACATTAGAATGGAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 ATATAGATAATGGTACATTCATATAAACATGATATTATTTACTAATTAAAACATACCA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 GAATAAATTCTAGTATATTCATACAAATGCAAGAGCAATGAAAATGAAACTCCTGCTA 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 39697; 3071pp + Sequence Listing; English.
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                                   2000US-0249264P
2000US-0249265P
2000US-0249209P
2000US-0249300P
2000US-0250160P
2000US-0250180P
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2000US-0251990P
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Best Local Similarity 59.0
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483426/52.
                                        17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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ABN85752 standard; DNA; 173810

ABN85752

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BXXXEX

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04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0180628P.
26-MAR-2000; 2000US-0189874P.
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19-MAY-2000; 2000US-0199123P.
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20-JUN-2000; 2000US-0209467P.
20-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0215135P.
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11-JUL-2000; 2000US-0220963P.
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26-JUL-2000; 2000US-0220963P.
14-AUG-2000; 2000US-0225266P.
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23-AUG-2000; 2000US-0227009P.
30-AUG-2000; 2000US-0228924P.
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2000US-0231413F.
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                                   WO200155367-A1
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01-SEP-2000;
05-SEP-2000;
     Homo sapiens,
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01-SEP-2000;
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21-SEP-2000;
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     42936 Aridiziarakakangakaratarakan 42995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a nucleic acid molecule (I) encoding a Can 1 polypeptide. The Can 1 nucleic acid molecule is used to diagnose or treat infertility or premature ovarian failure or Sertoli Cell only syndrome in a mammal. The present sequence is that of a mouse Can 1 encoding chromosome 11 BAC clone RP23-27018 of the invention. Note: The present sequence is not given in the printed specification but was obtained through the GenBank reference ACO83381S
                                                                                                                                                                                                                                                                                                                                                                                                         A nucleic acid molecule (I) encoding a Can 1 polypeptide used in treating infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vunerary; anticonvulsant; antibacterial; antifungal; antiparaaitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 AAGAACAGAGAGAGAGATTCAAATGTCCTTACAGAAGACTGATTATATAGATA 477
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                            Mouse; Can 1; antiinfertility; gynaecological; infertility; premature ovarian failure; menopause; Sertoli Cell only syndrome; BAC clone RP23-27018; GenBank reference AC083815; chromosome 11; d
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Mouse chromosome 11 BAC clone RP23-270L8 SEQ ID NO 10,
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57.6%; Pred. No. 5.6;
cive 0; Mismatches
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                                                                                                                                                                                                    02-NOV-2001; 2001US-00003806
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                                                                                                                                                                                                                                                                                                                                       Bishop CE, Agoulnik AI,
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les 72; Conservative
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                                                                                                 Mus musculus.
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2000US-0236367P.
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                                      2000US-0236802P.
2000US-0237037P.
2000US-0237038P.
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2000US-0237040P.
2000US-0239935P.
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2000US-0240960P.
2000US-0241221P.
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05-DEC-2000; 2000US-0251030P.
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(HUMA-) HUMAN GENOME SCI INC

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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or amaliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues and isclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, carthritis and ulcerative colitis, (c) cardiovascular disoraese, such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases e.g. ceebral anoxia and epilepsy; and (f) infectious diseases such as viral, chis patent did not form part of the printed specification, but was contented another the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5908 GAGGAACAAAAGCTTAAAGACAATCAAAATGTCCTTTAATAGAGGACTGTCTAAATCAAT 5967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral; antiallergic; hepatotropic; antidiabetic; antiinfiammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiousscular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 GAAGAACAGGAGACAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11027 BP; 2851 A; 2179 C; 2539 G; 3458 T; 0 U; 0 Other;
                                                                                                                                                                                 Example 2; SEQ ID NO 3655; 781pp + Sequence Listing; English.
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                 Ruben SM;
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                    Barash SC,
                                                          WPI; 2001-451937/48.
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                    Rosen CA,
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PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237037P.
PR 13-OCT-2000; 2000US-0237040P.
PR 20-OCT-2000; 2000US-0237040P.
PR 20-OCT-2000; 2000US-0241765P.
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PR 20-OCT-2000; 2000US-0246178P.
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PR 20-OCT-2000; 2000US-024611P.
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PR 20-OCT-2000; 2000US-0249218P.
PR 20-OCT-2000; 2000US-0249218P.
PR 20-OCT-2000; 2000US-0249218P.
PR 20-OCT-2000; 2000US-0249218P.
PR 20-OCT-2000; 2000US-0249218P.
P

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal

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The invention relates to novel genes (AAL14669-AAL17666) and proteins

(ABB03087-ABB04109) associated with the musculoskeletal system useful for
preventing, treating or ameliarating medical conditions e.g. by protein
or preventing, treating or ameliarating medical conditions e.g. by protein
or gene therapy. The genes are isolated from a range of human tissues
disclosed in the specification. The nucleic acids, proteins, antibodies
and (ant)agonists are useful in the diagnosis, treatment and prevention
of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
clung, or urogenital, (b) immune discorders e.g. Addison's disease,
allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
allergies, autoimmune haemolytic acardivascular disorders such as
mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
cerebral anoxia and parastic infections. Note: The sequence data for
this patent did not form part of the printed specification, but was
obtained in electronic format directly from WIPO at
the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11027. BP; 2851 A; 2182 C; 2537 G; 3457 T; 0 U; 0 Other;
                                                                    Example 2; SEQ ID NO 3654; 781pp + Sequence Listing; English.
cancers and also for testing and detection e.g. diagnosis.
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5908 GAGGAACAAAAGCTTAAAGACAATCAAAATGTCCTTTAATAGAGGACTGTCTAAATCAAT 5967 417 GAAGAACAGGAGACAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGAT 476 Gaps . 0 7.1%; Score 40; DB 4; Length 11027; ilarity 55.9%; Pred. No. 2.7; Conservative 0; Mismatches 60; Indels Ouery Match Best Local Similarity Matches 76; Conserva'

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537 ACCICGAGCCGCTAGT 552

6028 TGAGGGAGCTTTCAGT 6043

Search completed: August 14, 2004, 19:13:46 Job time : 287.474 secs

Sequence Sequence

Sequence 10, Apply Sequence 114034, Sequence 114034, Sequence 114035, Sequence 114035, Sequence 114035, Sequence 116036, Apply Sequence 1606, Apply Sequence 1606, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 2658, Apply Sequence 18, Apply Sequence 1265, Apply Sequence 1

18, Appl 1265, Ap 1972, Ap 160076,

Sequence 1 Sequence 1 Sequence 1

Sequence

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US-10-082-830-99

Sequence 99, Application US/10082830

Publication No. US20330077604A1

GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Salcada, Susana
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
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APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Compositions and Proteins
TITLE OF INVENTION: Compositions and Proteins
CURRENT FILING DATE: 2001-10-29
MUNGBER OF SEQ ID NOS: 22.
SOFTWARE: PatentIn Ver. 2.1
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100.0%; Score 563; DB 15;
100.0%; Pred. No. 4.1e-147;
Ative 0; Mismatches 0;
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Matches 563; Conservative
                                                                              ORGANISM: Homo sapiens
US-10-082-830-99
  SEQ ID NO 99
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                                                                                                                                          August 14, 2004, 19:13:54 ; Search time 319.797 Seconds (without alignments) 8638.053 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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3 US-10-087-192-1498
0 US-09-76-891-10207
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5 US-10-21-455-2130
6 US-10-292-798-1369
6 US-10-292-120056
6 US-10-085-117-334
0 US-09-962-436-231
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US-10-242-535A-16076
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                                                                                                                                                                                                                                                                                                                                                                       3225727 seqs, 2453303834 residues
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Maximum Match 100%
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Perfect score:
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Length 563; Indels 9

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                                                     AGTCTCCATTGAGCCATGAACTGTGAGCACCTGGCATTTAAGCATGAAGAGTAGGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10207, Application US/09764891
; Publication No. US20030077808A1
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10207
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US-10-205-428-1006/c
US-10-205-428-1006, Application US/10205428
; Fublication No. US20030108907A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA117C1
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Pred. No. 1.1;
0; Mismatches 56;
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Matches 76; Conservative
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                                                          240
                                                                                                                  300
                                                                                                                                             300
                                                                                                                                                                                            540
                                                                                                                                                                           GATTATCAGTTAAATACTTCTGGACCAAAGAAGACCTTGAAATCCTGGCTCGGTGATGTA 360
                                                                                                                                                                                                                                  AACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATG 480
                                                                                                                                                                                                                                                                                                                    421 AACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATG 480
                                                                             rccrarrirccrraaarrracragaagrgaggcrccaagaacracagaaaragaaggaa
                                                                                                                  TATGGTAGGGACTGGAGTAGGCAGCATTCCAGGAAAGGATCTCAGAGGTCAGAAACAATA
                                                                                                                                                                                                                                                                                                                                                   ATCAAATCTTAGGATGTATTACTTCCAAGGCGGTTAAACTTATTCAAGATTGACTGAGTC
                                                          AGTOTOCOATTGAGCCATGAACTGTGAGCACCTGGCATTTAAGCATGAAGAGTAGGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGTACATCTTGGCTGTGGATGGAAATTTGACATACTTTTTATTTTCTTTACCTGTTACAT
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99.6%; Pred. No. 4.2e-131;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGCCGCTAGTCTCGAGTCTAG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                   CGAGCCGCTAGTCTCGAGTCTAG 563
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| LOCATION: (1)...(330973)
| OTHER INFORMATION: n = A,T,C or G
| US-10-087-192-1498
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US-10-087-192-1498
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Best Local
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WESULO 292-798-1369/c

Sequence 1369, Application US/10292798

Sequence 1369, Application US/10292798

PUBLICANT NO. US20030235833A1

GENERAL INPORMATION:

APPLICANT: SAMIKO

APPLICANT: ABURATANI, HIROYUKI

TILLE OF INVENTIONS GH435/166

CURRENT APPLICATION NUMBER: US/10/292,798

CURRENT FILING DATE: 2002-11-13

FRICR FILING DATE: 2002-11-13

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SEQ ID NO 1369

LENGTH: 744602
                                                                                                                                                                                             422 ACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGG 481
                                                                                                                                                                                                                                                0
                OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                           Score 42; DB 15; Length 16766;
Pred. No. 2.2;
0; Mismatches 45; Indels 0
                                                                                         Query Match 7.5%;
Best Local Similarity 60.5%;
Matches 69; Conservative
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(235514)..(235560)
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(25640)..(25677)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS. (201)..(246)
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                                US-10-311-455-2130
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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LOCATION:
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| Sequence 2130, Application US/10311455 |
| Sequence 2130, Application US/203143606A1 |
| GENERAL INFORMATION |
| APPLICANT: OLEK, Alexander |
| APPLICANT: OLEK, Alexander |
| APPLICANT: DIERDRANCK, Christian |
| APPLICANT: DIERDRANCK, Christian |
| APPLICANT: DIERDRANCK, Christian |
| APPLICANT: DIERDRANCK, Christian |
| TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ |
| TITLE OF INVENTION: Ortosine methylation |
| TITLE OF INVENTION: Ortosine methylation |
| TITLE OF INVENTION: Ortosine methylation |
| TITLE OF INVENTION: Ortosine methylation |
| FILE REFERENCE: 5013.1014 |
| CURRENT APPLICATION NUMBER: DC1/EP01/07537 |
| PRIOR PELING DATE: 2000-06-30 |
| PRIOR PELING DATE: 2000-06-30 |
| PRIOR PELING DATE: 2000-06-30 |
| PRIOR FILING DATE: 2000-09-01 |
| WUUMBER OF SEQ ID NOS: 2424 |
| SEQ ID NO 2130 |
| LENGTH: 16766 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 GTCCTTACACAGAAGACTGATTATATAGATAATGGTACATTCATATAAACATGATATATT 506
CURRENT APPLICATION NUMBER: US/10/205,428

FRIOR APPLICATION NUMBER: 09/764,892

PRIOR APPLICATION NUMBER: 09/764,892

PRIOR APPLICATION NUMBER: 00/130,065

FRIOR APPLICATION NUMBER: 00/180,628

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR APPLICATION NUMBER: 60/214,886

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR PLING DATE: 2000-07-11

PRIOR PLING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR APPLICATION NUMBER: 60/225,458

PRIOR APPLICATION NUMBER: 60/217,496

PRIOR PLING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/217,496

PRIOR PLING DATE: 2000-07-11

PRIOR PLING DATE: 2000-07-11

PRIOR FILING DATE: 2000-07-11

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-07-14

PRIOR PLING DATE: 2000-08-14

PRIOR FILING DATE: 2000-07-14

PRIOR PLING DATE: 2000-08-14

PRIOR PLING DATE: 2000-08-14

PRIOR PLING DATE: 2000-08-14

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PRIOR PLING DATE: 2000-08-14
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Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.5%;
Best Local Similarity 57.6%;
Matches 76; Conservative (
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ORGANISM: Artificial Sequence
FEATURE:
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; ORGANISM: Homo sapiens
US-10-205-428-1006
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418 AAGAACAGGAGACAGAGACAATTCAAATGTCCTTACACAGAAGACTGATTATAGATA 477
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Induction and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-34

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-10-23

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PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
USALID-027-032-120056/
USALID-027-032-120056/
USALID-027-032-120056/
Publication No. US20020198371A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| FILE REFERENCE: 10827.129 |
| CURRENT APPLICATION NUMBER: US 60/128,006 |
| PRIOR PELING DATE: 2000-07-12 |
| PRIOR PELING DATE: 2000-07-12 |
| PRIOR PELING DATE: 2000-07-12 |
| PRIOR PELING DATE: 2000-03-29 |
| PRIOR PELING DATE: 2000-03-29 |
| PRIOR PAPLICATION NUMBER: US 60/198,218 |
| PRIOR PELING DATE: 2000-02-24 |
| PRIOR PELING DATE: 2000-02-24 |
| PRIOR PELING DATE: 1999-11-28 |
| PRIOR PELING DATE: 1999-11-28 |
| PRIOR PELING DATE: 1999-11-28 |
| PRIOR PELING DATE: 1999-09-28 |
| PRIOR PELING DATE: 1999-09-28 |
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| PRIOR PELING DATE: 1999-09-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 ATGGTACATTCATATAACATGATATTTTACTAATTAAAA 518
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120056
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Publication No. US20030204075A9
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Best Local Similarity
Matches 64; Conserv
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GRGANISM: Human
US-10-027-632-120056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; Score 42; DB 16; Length 744802; 66.7%; Pred. No. 18; ive 0; Mismatches 30; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified base
LOCATION: (332992)...(332992)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: modified base
LOCATION: (619880)
COTATION: (619880)
COTATION: (7, c, g, unknown or other US-10-292-798-1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified base
LOCATION: (332935) ... (332935)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           609677 TGCATCTATTCATGAGATATTTAGATTTA 609648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g, unknown or other
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THER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COCATION: (310089) ... (310188)
THER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g, unknown or other
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LOCATION: (293951)..(294050)
JTHER INFORMATION: a, t, c, g, unknown or
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LOCATION: (362002)..(362101)
OTHER INFORMATION: a, t, c, g,
                          CDS (409204)..(409669)
                                                                                                                                                                                                                                              CDS (472204)..(472330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified base
LOCATION: (57122)...(57221)
OTHER INFORMATION: a, t, c,
                                                                                                                                                                     (428381)..(428396)
                                                                                                                                                                                                                                                                                                                                                                                            (714252)..(714355)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified base
LOCATION: (51812)...(51911)
OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
(714447)..(714529)
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                  NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
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RESULT 7

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Sequence 273, Application US/09964824A

Patent No. US20020102531A1

GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat:
TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-73

CURRENT APPLICATION NUMBER: US/09/964,824A

CURRENT APPLICATION NUMBER: US/60/236,033

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 583

SOFFWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                   159637 ATTGTTCAAAATAACAAAAGATTGGAAAGAAGGCAAATATCCTTGAGTAGAAGACTGATG 159696
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                                                                                                                                                                                                                                                      409 ATAGGGCTGAAGAACAGGAGACAAGACAATTCAAATGTCCTTACACAGAAGACTGATT
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                                                                                                                                                       Length 167343;
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Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer;
FILE REPERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                       DB 9;
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                                                                                                                                                    Score 41.2; Di
Pred. No. 13;
0; Mismatches
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                                                                                                                                                                            Best Local Similarity 67.4
Matches 58; Conservative
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Best Local Similarity 67.4
Matches 58; Conservative
; SEQ ID NO 281

: LENGTH: 167343

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-962-436-281
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CRGANISM: Homo sapiens
US-09-964-824A-273
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APPLICANT: Soppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                    577 AATAACCCCAAACAGTAAACAATCCAAAGACCCATTCACAGGTGAAAGAATAAATT 518
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7.4%; Score 41.8; DB 16; Length 154817;
Best Local Similarity 63.4%; Pred. No. 8.6;
Matches 64; Conservative 0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 334, Application US/10085117
| Publication No. US2003023234A1
| GENERAL INFORMATION:
| APPLICANT: Morris, David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER |
| FILE REFERENCE: 529452000121 |
| CURRENT APPLICATION NUMBER: US/10/085,117 |
| CURRENT FILING DATE: 2002-02-27 |
| PRIOR APPLICATION NUMBER: US 09/798,586 |
| PRIOR FILING DATE: 2001-03-02 |
| NUMBER OF SEQ ID NOS: 361 |
| SOFTWARER FASELES for Windows Version 4.0
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0
                                                                                                                               Length 915;
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                                                                                                                          Score 41.8; DB 16;
Pred. No. 0.49;
0; Mismatches 37;
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COTHER INFORMATION: n = any nucleotide
US-10-085-117-334
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Patent No. US20020081301A1
                                                                                                                            Query Match
Best Local Similarity 63.4%;
Matches 64; Conservative C
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                          ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-085-117-334/c
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LENGTH: 154817
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     LENGTH: 915
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Publication No. US20040037841A1;
Publication No. US20040037841A1;
Publication No. US20040037841A1;
APPLICANT: ChondroGene Inc.;
APPLICANT: ChondroGene Inc.;
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002;
CURRENT APPLICANTION NUMBER: US/10/085,783A;
CURRENT FILING DATE: 2002-28;
PRIOR APPLICATION NUMBER: US 60/275,017;
PRIOR APPLICATION NUMBER: US 60/275,017;
PRIOR PILING DATE: 2001-07-13;
PRIOR FILING DATE: 2001-07-13;
PRIOR FILING DATE: 2001-07-13;
PRIOR FILING DATE: 2001-07-14;
PRIOR FILING DATE: 2001-07-15;
PRIOR FILING DATE: 2001-03-12;
SPRIOR SPILING DATE: 2001-03-12;
PRIOR FILING DATE: 2001-03-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 ATTATGCTTAACAGCCCCAAACTGGAAATAATTCAAATGTCCATTAACATTAGAATGGAT 180
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Publication No. US20040013663A1

GENERAL INFORMATION

APPLICANT: ChondroGene Inc.

APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT PILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085,783

PROPERIOR TILING DATE: 2002-02-88

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13
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                                                                                                                                                                                                                                                                                              Query Match 7.3%; Score 41; DB 17; Length 97415; Best Local Similarity 61.9%; Pred. No. 11; Matches 65; Conservative 0; Mismatches 40; Indels 0
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7.1%; Score 40.2; DB 13; Length 414;
Best Local Similarity 59.0%; Pred. No. 0.88;
Matches 69; Conservative 0; Mismatches 48; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48497 ATATGGTACATTACACAATGGAGTACTACTTGCTATTAAAAACA 48541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476 TAATGGTACATTCATATAAACATGATATTTACTAATTAAAACA 520
                                    FEATURE:

NAME/KEY: misc feature
LOCATION: (1)...(97415)

OTHER INFORMATION: n = A,T,C or G
US-10-322-281-287
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-085-783A-16076/c
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US-10-242-535A-16076/c
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 ATTATGCTTAACAGCCCCAAACTGGAAATAATTCAAATGTCCATTAACATTAGAATGGAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 ATATAGATAATIGGTACATICATATAAACATGATATATTTACTAATTAAAACATACCA 525
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| Sequence 622, Application US/10240425
| Publication No. US20040033502A1
| Publication No. US20040033502A1
| GENERAL INFORMATION:
| APPLICANT: Williams, Amanda
| APPLICANT: Milliams, Amanda
| APPLICANT: Lord, Reginald V. APPLICANT: APPLICANT: Ord, Reginald V. APPLICANT: APPLICANT: APPLICANT: APPLICANT: Wetzel, Uwe
| APPLICANT: Wockley, Useeph G. APPLICANT: Wockley, Useeph G. INVENTION: Gene Expression Profiles in Esophageal Tissue FILE REFERENCE: 44921-5026
| TILLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue FILE REFERENCE: 44921-5026
| CURRENT FILING DATE: 2002-09-30 |
| PRIOR FILING DATE: 2001-03-28 |
| PRIOR APPLICATION NUMBER: US 60/193,446 |
| PRIOR APPLICATION NUMBER: US 60/193,446 |
| PRIOR FILING DATE: 2000-09-31 |
| SEQ ID NO 622 |
| LENGTH BEALTH Ver. 2.1 |
| LENGTH BEALTH Ver. 2.1 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.1%; Score 40.2; DB 16; Length 414; Best Local Similarity 59.0%; Pred. No. 0.88; Matches 69; Conservative 0; Mismatches 48; Indels 0
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PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
LENGTH: 414
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-242-535A-16076
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION 0 PATA:
APPLICATION DATA:
PRICH APPLICATION DATA:
PRICH APPLICATION DATA:
PILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: CHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 5.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner STEET: 1800 Diagonal Road, Suite 500
US-09-621-976-2813

US-09-149-476-112

US-09-539-33D-1

US-09-679-403-1

US-09-331-359-1

US-10-204-708-39

US-09-107-532A-290

US-09-107-532A-290

US-09-107-532A-290

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US-09-107-532A-290

US-09-107-532A-290

US-09-107-532A-290

US-09-107-532A-290

US-09-107-532A-290

US-09-832-893-66

US-08-832-893-66

US-08-832-893-66

US-09-956-1111-352

US-09-978-985-11

US-10-027-985-11
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⊢,
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FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) 836-9300
TELEFRAX: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
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; Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
    6.1 1832
6.1 31608
6.1 31608
6.1 31608
6.0 19513
6.0 19513
6.0 35100
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EDNESS: single
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US-08-232-463-14
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STATE: VI
COUNTRY:
                                                                              Query Match
     00000 00
                                                                                      August 14, 2004, 11:00:56 ; Search time 54.0891 Seconds (without alignments) 5776.350 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                         /cgn2 6/ptodata/2/ina/5A COMB.seq:*
/cgn2 6/ptodata/2/ina/5B COMB.seq:*
/cgn2 6/ptodata/2/ina/6A COMB.seq:*
/cgn2 6/ptodata/2/ina/6B COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS COMB.seq:*
                GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-232-463-14
US-09-750-580-1
US-10-264-708-18
US-10-160-180-3
US-09-741-150-3
US-08-616-844-36
US-08-59-616-844-36
US-08-98-59-618-36
US-08-98-59-618-36
US-08-98-573-6
US-08-98-573-6
US-08-98-573-6
US-08-98-618-36
US-08-98-773-36
US-08-98-773-36
US-08-925-747-36
US-08-925-748-36
US-08-925-748-36
US-08-925-748-36
US-08-925-748-36
US-08-925-748-36
US-08-925-76-11
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US-08-925-76-11
US-08-925-88-11
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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US-10-204-708-14
US-10-204-708-55
                                                                                                                                                                                                                                   682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
                                                                nucleic search, using sw model
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Maximum Match 100%
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length: 2000000000
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Match Length
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OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
TOCATION: 14992..15012
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OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460.15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
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NAME/KEY: misc. feature
LOCATION: 15969...17969
OTHER INFORMATION: 3'regulatory region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAMES, NAMES TO SECULD STATION: 77058
OTHER INFORMATION: 20-853-415 : NAMES/KEY: primer bind CCATION: 929.949
OTHER INFORMATION: 20-828.pu
NAMES/KEY: primer bind LOCATION: 1357.1377
OTHER INFORMATION: 20-828.rp cc
NAMES/KEY: primer bind COTHER INFORMATION: 20-828.rp cc
NAMES/KEY: primer bind COTHER INFORMATION: 20-828.rp cc
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OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp c
NAME/KEY: primer_bind
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: 45442
OTHER INFORMATION: 20-842-115
NAME/KEY: allele
LOCATION: 77058
                                                                                                                                                                                                                                                                                                                                                                                                                            JOCATION: 1239
THER INFORMATION: 20-828-311
NAME/KEY: allele
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CCATION: 42218
THER INFORMATION: 20-841-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 12347
OTHER INFORMATION: 17-42-319
NAME/KEY: allele
LOCATION: 15241
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LOCATION: 45863. 45883
THER INFORMATION: 20-842.rp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: 17-41-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION: 45328..45347
WHER INFORMATION: 20-842.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCATION: 76644..76664
THER INFORMATION: 20-853.pu
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
                                                                                                            OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                          14271..15968
                                                                                       13470..13526
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-c, Aymeric

-gualeret, Lydie

Egbete-Reed, Dana

-i. Salter-Cid, Linisa

- OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

-LE REPERENCE: 99.162. CH

- OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

- OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

- OF INVENTION: METHOD AND COMPOSITIONS FOR THIRD AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIONS AND COMPOSITIO
                                                                                                                              135 AATTTACTAGAAGTGAGGCTCCAAGAACTACAGAAAATAGAAGGAAAGTCTCCATTGAGC 194
                                                                                                                                                                                                      195 CATGAACTGTGAGCACCTGGCATTTAAGCATGAAGAGTAGGGCTTCTATGGTAGGGACTG 254
                                                                                                                                                                                                                                                                                                                   GAGTAGGCAGCATTCCAGGAAAGGATCTCAGAGGTCAGAACAATAGATTATCAGTTAAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                  315 TACTTCTGGACCAAAGAACCTTGAAATCCTGGCTCGGTGATGTATACATATTTAATAC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 ACAATGAGAAGCTCCTTGAGGGTGAGTGAGAGTGATAGGGCTGAAGAACAGGAGACAGAA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 GACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGGTACATTCATATAA 494
                                    Gaps
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0
      Best Local Similarity 1.9%; Pred. No. 2.2e-05;
Matches 7; Conservative 218; Mismatches 141; Indels
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LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
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generic 18, Application US/10204708

patent No. 6677731

GENERAL INFORMATION:

APPLICANT: DIBPENBROCK, Christian
APPLICANT: DIBPENBROCK, Christian
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APPLICANT: DIBPENBROCK, Christian
APPLICANT: DIBPENBROCK, Christian
APPLICANT: DISPENBROCK, Christian
APPLICANTON: DY Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT FILING DATE: 2003-65-66
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
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PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: DE 10043826.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 GATAGGGCTGAAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGAT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GATTAATCATAATAGCACAAAACTGGAAGCAATCTAAATGTCCATTAACTGGTGAGTGGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 TATATAGATAATGGTACATTCATATAAACATGATATTTTACTAATTAAAACATACCAA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 TAAACCAAATGTGGTATATACATACAACTGAATACTATTCCATTAATAAAAAGGRACAAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2482 AAACAAAATAAATAAAAAATCAATAACATAACAAAATATCAAAATAAACGTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 AGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATAATGGTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37.4; DB 4; Length 408;
Pred. No. 0.23;
0; Mismatches 51; Indels
                                                 APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8793
APPLICANT: Dumas Milne Edwards, J.B
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 57.1 68; Conservative
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
COGANISM: Homo sapiens
US-09-621-976-8793
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Best Local S
Matches 68
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                                                                                                                                                                                                                                                                                                        LOCATION: 1242...15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 49199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 45423...45441
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423...45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45423...45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 70039...77057
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039...77057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 77059.77077
OTHER INPORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227.1251
OTHER INPORMATION: 20-828-311.probe
LOCATION: 12335.12359
INFORMATION: 20-828-311.mis complement
                        OTHER INFORMATION: 17-42-319.mis
NAME/KEY: priner bind
LOCATION: 12348.12366
OTHER INFORMATION: 17-42-319.mis complement
LAME/KEY: priner bind
LOCATION: 1522
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; Sequence 8793, Application US/09621976
; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: 20-841-149.probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 12335..12359
OTHER INPORMATION: 17-42-319.probe
MAMA/KEY: misc_binding
LOCATION: 15229..15239
OTHER INFORMATION: 17-41-250.probe
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                                                                                                                                                                                                                           LOCATION: 15222. 15240
OTHER INFORMATION: 17-41-250.mis
MAMB/KEY: primer.bind
10020170N: 15242.15260
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24899 GACAGCTTTATTTTAATAGCCAAAAACTGAAAACAACCAAATGTCTATCAACAGATG 24840
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                                                                                                                                                                                                              462 ACTGATTATATATAGATAATGGTACATTCATATAAACATGATATATTTACTAATTAAAACAT 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/08480994

Patent No. 5834248

PATENT INFORMATION:

APPLICANT: FALB, DEAN A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CITY: New York
STATE: New York
                                                                                                         402 GAGAGTGATAGGGCTGAAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAAG
  DB 4; Length 112132;
                                                    .
0
                                                  59; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,994
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: US 08/485,573
ATIONER/AGENT INFORMATION:
  6.3%; Score 35.6; DB ilarity 54.6%; Pred. No. 6.2; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 7853 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090 TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
                                                                                                                                                                                                                                                                                                                                                                       24779 AACAAATTAC 24770
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2911
                                                                                                                                                                                                                                                                                                                     522 ACCAACACAC 531
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EDNESS: both
                           Similarity
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10036-2711
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FEATURE:
Query Match
Best Local Simi:
Matches 71; (
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LOCATION:
FEATURE:
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, LOCATION:
US-08-480-994-36
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| Sequence 3, Application US/10160187 |
| Sequence 3, Application US/10160187 |
| Sequence 3, Application US/10160187 |
| Sequence 3, Application US/10160187 |
| Patent No. 6620607 |
| GENERAL INFORMATION: ISOLATED HUMAN PROTEASE PROTEINS, ITLLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, ITLLE OF INVENTION: USSS THEREOF |
| TITLE OF INVENTION: USSS THEREOF |
| TITLE OF INVENTION: USSS THEREOF |
| TITLE OF INVENTION: USSS THEREOF |
| TITLE OF INVENTION: USSS THEREOF |
| TITLE OF INVENTION NUMBER: US/10/160,187 |
| CURRENT APPLICATION NUMBER: US/25,410 |
| PRIOR FILING DATE: 2000-11-22 |
| PRIOR PILING DATE: 2000-11-22 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTWARE: FASELSEQ for Windows Version 4.0 |
                                                                                                                                              Sequence 3, Application US/09741150
Patent No. 643669
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION USES THEREOF
GURRENT APPLICATION NUMBER: US/09/741,150
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24899 GACAGCTTTATTTTAATAGCCAAAAACTGAAAACAACCCAAATGTCTATCAACAGATG 24840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 GAGAGTGATAGGGCTGAAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 ACTGATTATATAGATAATGGTACATTCATATAAACATGATATATTTACTAATTAAAACAT 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.3%; Score 35.6; DB 4; Length 112132; Best Local Similarity 54.6%; Pred. No. 6.2; Matches 71; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
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LOCATION: (1)...(112132)

OTHER INFORMATION: n = A,T,C or G

US-10-160-187-3
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                         2362 TTTAATC 2356
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 112132
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LENGTH: 112132
                                                                                                                                  US-09-741-150-3/c
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821 AACAGCCAAAGAAGGAAGCAACCCAAATGTCCATTAGCTGATAAATGGATAATGAAAT 880
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Patent No. 5882291
Patent No. 5882291
Patent No. 5882291
Patent No. 5882291

APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                    478 AIGGIACATICATATAAACAIGATATATITACTAATTAAAACATACCAACACACA
                                                                                                                                                                                                       Gaps
                                                                                                                                           Score 35.4; DB 2; Length 3083;
Pred. No. 1.8;
0; Mismatches 61; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDITOM TYPE: READABLE FORM:
MEDITOM TYPE: RIPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,654
FILING DATE: 09-FEB-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
RESTRANION NUMBER: 30,742
RESTRANION NUMBER: 7853-041
TELECOMMUNICATION NUMBER: 7853-041
                                                                                                                                        Query Match 6.3%;
Best Local Similarity 54.1%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 CCTCGAGCCGCTA 550
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TELEPHONE: (212) 869-8864
                                misc_feature
2911
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NAME/KEY: misc_feature
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STRANDEDNESS: both
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STATE: New York
COUNTRY: USA
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-616-844-36
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LOCATION:
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Patent No. 584978

Patent No. 584978

Patent No. 584978

TITLE OF INVENTION: COMPOSITION AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSE: PRINIE & EDMONDS

STREET: 1155 Avenue of the Americas

CITY. New York

COMPUTER: LOS AVENUE OF THE PLOYON AND ALL SOND ADDRESSES

COMPUTER: LOS AVENUE OF THE PLOYON AND ALL SOND ADDRESSES

COMPUTER: LOS AVENUE OF THE SEQUENCE ADDRESSES

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COMPUTER: LOS AVENUE ADDRESSES

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                                                                                                                                                                                                                                                                                                881 ATGGTACGTCCGAAGAATGGAATATCATTCACCCATGAAAAAGAAGAAGTCCAGCACCA 940
                                                                                                                                                                                                                                          478 AIGGIACATICATATAAACAIGATAITIACTAATIAAAACATACCAACACACACACA
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                          DB 2; Length 3083;
                 Query Match 6.3%; Score 35.4; DB 2; Length 3 Best Local Similarity 54.1%; Pred. No. 1.8; Matches 72; Conservative 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                           538 CCTCGAGCCGCTA 550
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EDNESS: both
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STRANDEDNESS:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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US-08-944-668A-36

Sequence 36, Application US/08944868A

Sequence 36, Application US/08944868A

Patent No. 6018025

TETLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
ADDRESSE:
ADDRESSE:
PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas
CONTREPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
PENNIE & EDMONDS

STATE: New York
CONTREP: PENNIE & EDMONDS

STATE: New York
CONTREP: PENDIE FORM:
COMPUTER READABLE FORM:
COMPUTER: 1036-2711

COMPUTER: Datentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/944,868A
                                                                                                                                                                                                                                                                                 881 AIGGIACGICCGAAGAAIGGAAIAICAITCAITCACCCAIGAAAAAGAAGGAAGICCAGCACA 940
                                                                                                                                                              418 AAGAACAGGAGACAGAAGACAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
                                                                                                                                                                                                    821 AACAGCCAAAGAAGGAAGCAACCCAAATGTCCATTAGCTGATAAATGGATAAAT 880
                                                                                                                                                                                                                                              478 AIGGIACAITCAIAIAAACAIGAIAITIACIAAITIAAAAACAIACCAACACACACACAACA 537
                                                                                                                         Gaps
                                                                                                                         ;
                                                                             Query Match
6.3%; Score 35.4; DB 2; Length 3083;
Best Local Similarity 54.1%; Pred. No. 1.8;
Matches 72; Conservative 0; Mismatches 61; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRICR APPLICATION DATA:
APPLICATION UNMBER: US 08/386,844
FILING DATE: 10-FEB-195
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFREENCE/DOCKET NUMBER: 30,742
REFREENCE/DOCKET NUMBER: 30,742
TELEPONE: (212) 790-909
TELEPONE: (212) 869-8644
TELEPONE: (212) 869-8644
TELES: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,654
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                      538 CCTCGAGCCGCTA 550
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misc_feature
2911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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LOCATION:
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  ; NAME/KEY:
; LOCATION:
US-08-485-573-36
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                                                                                                                                                                                                                 418 AAGAACAGAACAGAAGACAATICAAATGICCTTACACAGAAGACTGATTATAAGATA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/08485573
Sequence 36, Application US/08485573
Patent No. 5968770
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                             Score 35.4; DB 2; Length 3083; Pred. No. 1.8; 0; Mismatches 61; Indels 0
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COUNTRY: USA

ZIP: 10036-2711

COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

OPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ParentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,573

FILING DATE: 07-UNM-1995

FILING DATE: 07-UNM-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07-UN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-032
TELECHONE: (212) 790-9990
TELECHONE: (212) 869-8864
                                                                                                                                  Query Match (4.3%; Best Local Similarity 54.1%; Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              941 AAACGTGCTACAA 953
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                                                    misc_feature
2911
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LOCATION: 16
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STRANDEDNESS: both
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      LOCATION: 730
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LOCATION:
FEATURE:
                              ; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-599-654-36
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US-08-485-573-36
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418 AAGAACAGGAGACAAATTCAAATGTCCTTACACAGAAGACTGATTATATAGATA 477
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Sequence 36, Application US/08925743

Sequence 36, Application US/08925743

GENERAL INFORMATION:

Patent No. 6044558

GENERAL INFORMATION:

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TILLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

CORRESPONDENCE ADDRESS:

ADDRESSEE: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                         Query Match
6.3%; Score 35.4; DB 3; Length 3083;
Best Local Similarity 54.1%; Pred. No. 1.8;
Matches 72; Conservative 0; Mismatches 61; Indels 0
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/925,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRICATION NUMBER: 08/485,573
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: COLL22!, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-03:
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 harr
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TELEFAX: (212) 869-8864
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                  misc_feature
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                                                                                                                                                                    misc_feature
2911
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NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
US-08-944-423A-36
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Sequence 36, Application US/08944423A
Patent No. 6020463
GENERAL INPORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF SEQUENCES:
ADDRESSES:
ADDRESSES:
PENNIE & EDMONDS
STREET:
1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                        478 AIGGIACATICATATAAACAIGATAITTACTAATTAAAACATACCAACACACAACA
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                                                                                                                                                                    Length 3083;
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,423A
FILING DATE: 06-OCT-1997
                                                                                                                                                                 Score 35.4; DB 3;
Pred. No. 1.8;
                                                                                                                                                           Query Match
6.3%; Score 35.4; DB
Best Local Similarity 54.1%; Pred. No. 1.8;
Matches 72; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB.1996
FILING DATE: 09-FEB.1996
APPLICATION NUMBER: US 08/485,573
FILING DATE: UTN-07-1995
FILING DATE: UTN-07-1995
FILING DATE: UTN-07-1995
APTORNEY/AGENT INFORMATION:
NAME: CORUZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
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FEATURE:
NAME/KEY: misc_feature
' ^ aTION: 2911
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NAME/KEY: misc_feature
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COUNTRY: USA
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STRANDEDNESS:
                                                                     ; LOCATION:
US-08-944-868A-36
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Patent No. 6225084

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE NUMBER OF SEQUENCES:

ADDRESSEE: PENNIE & EDMONDS

STREET: 1155 Avenue of the Americas

GITY: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                    Query Match 6.3%; Score 35.4; DB 3; Length 3083; Best Local Similarity 54.1%; Pred. No. 1.8; Matches 72; Conservative 0; Mismatches 61; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/925,767
FILING DATE: 09-SEPT-1997
CLASSIFICATION NUMBER: US/08/925,767
FILING DATE: 09-SEPT-1997
PRIOR APPLICATION NUMBER: US/08/485,573
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INPERMATION:
NAME: COTULZ:, LAUTA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEY: (614) PENNIE
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGIH: 3083 base pairs
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STRANDEDNESS: both
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                   NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 Argerakcerckgaagaarargararcarreakceargaaaaagaakgaagrekgeageacka 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AUGGIACATICATATAAACATGATATTITACTAATTAAAACATACCAACACACAACA
                                                                                                                                                                                                                          DB 3; Length 3083;
                                                                                                                                                                                                                                                                                      61; Indels
                                                                                                                                                                                                                       Query Match 6.3%; Score 35.4; DB
Best Local Similarity 54.1%; Pred. No. 1.8;
Matches 72; Conservative 0; Mismatches
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LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 CCTCGAGCCGCTA 550
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STRANDEDNESS:
TOPOLOGY: unkr
   NAME/KEY: misc
LOCATION: 30
PEATURE:
                                                                                                ; NAME/KEY;
; LOCATION:
US-08-925-743-36
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MOLECULE TYPE: cDNA
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 10, 2004, 19:12:36 ; Search time 16 Seconds (without alignments) 288.575 Million cell updates/sec

US-10-082-830-224
248
1 FFFFLRQSFTLSQAGVAWH.....LPGSSDSRASASQSARITGV Title: Perfect score:

Sequence:

48

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database :

PIR 78:*
1: pir1:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	X-linked retinopat	artifact-warning s	artifact-warning s	artifact-warning s	probable thromboxa	thromboxane A-2 re	artifact-warning s	adducin homolog -	alpha-1C-adrenergi	gamma-adaptin homo	noncapsid protein		serine/threonine-s	methyltransferase		O	Н	_	_	en	hypothetical prote	Н			hypothetical prote		microtubule-associ	cellobiohydrolase	hypothetical prote
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	Score	144	103	83.5		79.5	79	74.5	67	62	61	19	59	59	58	28	58	57.5	7		56.5	. 56	56	26	52	55	55	55		4.
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Gaps

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Query Match
41.5%; Score 103; DB 4; Length 613;
Best Local Similarity 61.3%; Pred. No. 2.9e-05;
Matches 19; Conservative 4; Mismatches 8; Indels

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ALIGNMENTS

RESULT 1
X-linked retinopathy protein (C-terminal, clone XEH.8c) - human (fragment)
C,Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C. ACCESSION: A46010
o-monatios 1.7, 17.2, 17.2 A.Title: Identification and partial characterization of a candidate gene for X-linked re
A,Accesion: A46010
A Status: preliminary
A,Molecule Cype: Mucleic acid A:Residues: 1-100 <won></won>
A; Cross-references: GB: S58722; NID: 9299470; PIDN: AAB26149.1; PID: 9299471
A,Note: sequence extracted from NCBI backbone (NCBIN:129339, NCBIP:129340)
58.18;
best Local Shullarity 62.34; Fred. No. 2.26-11; Matches 30; Conservative 7; Mismatches 11; Indels 0; Gabs 0;
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Db 2 FFFFFFTESCSVAEAGVQWCDLGSLKSPPPGSSDSPASASRVAGITGM 49
CASULT 2 C40201
artifact-warning sequence (translated ALU class C) - human
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C.Date: 31 Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
R.Claverie, J.M.
personal communication, 1992
A, Reference number: A40201
A;Accession: C40201
A Molecule type: DNA
A;kesidues: 1-613 <cla> D.A]sassia I M</cla>
Airtaville, U.M. Genemice 1) 238-221 1002
oemonico 12, 050-041, 1202. A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall
MUID:92241891; PMID:1572661
A)contents: amondation C:Comment: This warning entry is a concentual translation in all 6 reading frames of c
)
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th

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R;Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-Schultz, K.; G.J.; Danganan, L.; Poundstone, P.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; At P.; Quan, G.; Kronmiller, B.; Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M. submitted to the EMBL Data Library, June 1998
A;Authors: Trong, S.; Kobayashi, A.; Olsen, A.S.; Carrano, A.V.
A;Description: Sequence analysis of a 3.5 Mb contig in human 19913.3 containing a serine A;Accession: T02670
A;Accession: Preliminary
A;Actual Data Library
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A;Reference number: A40201

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A;Reference number: A56194; MUID:95204505; PMID:7896853
A;Accession: A56194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nromboxane A-2 receptor, endothelial - human (fragment)
Species: Homo sapiens (man)
Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
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C;Speciee: Homo sapiens (man)
C;Date: 11-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 407;
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A,Residues: 1-407 <LAM>
A,Cross-references: EMBL:AC005175; NID:g3253116; PID:g3253117
C,Superfamily: prostaglandin E receptor EP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endothelial - human (fragment)
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llarity 85.0%; Pred. No. 0.0038;
Conservative 2; Mismatches 1
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C; Superfamily: prostaglandin E receptor EP1
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R; Claverie, J.M.
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                                                                                                                                                                                                                                                                                            artifact-warning sequence (translated ALU class F) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 11-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: F40201
R;Claverie, J.M.
personal communication, 1992
A;Reference number: A40201
A;Accession: F40201
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A;Accession: F40201
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
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C;Species: Homo sapiens (man)
C;Species: J.M.
Personal communication, 1992
A;Reference number: A40201
A;Species: Homo sapiens (man)
A;Species: Homo sapiens (man)
A;Residues: J.C.
Genomics: J.C.
Genomics: J.C.
A;Contents: annotation
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of cin-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th
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C;Species: Homo sapiens (man)
C;bate: 19-May-2000 #sequence_revision 19-May-2000 #text_change 15-Sep-2000
C;Accession: T02670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 FFFFFFFFFFVFVFEIGPCSDTPAGVQWQVLAHCSLNLLGSSDSPASVSRVAGITGM 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                   311 FFFFETESHSVTQAGVQWRDLGSLQAPPPG 341
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                                 FFFFFLRQSFTLSQAGVAWHDLGSLHPPLPG
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Best Local Similarity
Matches 16; Conserv
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A;Accession: C26104
A;Molecule type: DNA
A;Residues: 1-726 <CHE>
A;Cross-references: BMBL:M14363; NID:g333454; PIDN:AAB59845.1; PID:g808803; EMBL:M21972
C;Superfamily: parvovirus noncapsid protein
C;Keywords: noncapsid protein
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R;Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E.R.; Bates, R.C.
J. Virol. 60, 1085-1097, 1986
A;Title: Complete nucleotide sequence and genome organization of bovine parvovirus. A,Reference number: A26104; MUID:87061184; PMID:3783814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-adaptin homolog DKFZp564D066.1 - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serotonin receptor 6 - human
N;Alternate names: 5-hydroxytryptamine receptor 6 (5-HTR6)
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
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C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 726;
                                                                                                                                                                          Length 499;
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A,Cross-references: GDB:128088; OMIM:104221
A,Map position: 8p21-8p21.5
C,Superfamily: vertebrate rhodopsin
C,Keywords: alternative splicing; neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONWIFSENGVCWHCGGFIOPTPESDTDSDGDPDGAVAG 525
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Pred. No. 4.3;
1; Mismatches
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Pred. No. 8.7;
6; Mismatches 2:
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Pred. No. 6.1;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LRQSFTLSQAGVAWHDLGSLHPPLP 30
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                                                                                                                                                                                                                                                                                                                                                                                           446 LPGSRDSPASASQAAGTTG 464
                                                                                                                                                                                                                                                                                                                           29 LPGSSDSRASASOSARITG 47
                                                                                                                                                                       25.0%;
nilarity 73.7%;
Conservative 1,
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A,Residues: 1-522 <WAM>
A,Cross-references: EMBL:AL050025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 24.6%;
l Similarity 56.0%;
14; Conservative
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Best Local Similarity 30.0%;
Matches 12; Conservative
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C;Keywords: membrane trafficking
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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Ribing, D.; Parkhusz, S.M.; Lipshitz, H.D.

Proc. Natl. Acad. Sci. US.A. 90, 2512-2516, 1993

Proc. Natl. Acad. Sci. US.A. 90, 2512-2516, 1993

A; Recented mumber: A47397; MUID:93211992; PMID:7681599

A; Accession. A47397

A; Residues: preliminary

A; Molecule type: mRNA

A; Residues: 1-1156 oDIN

A; Residues: 1-1156 oDIN

A; Residues: Branch Source: embryo

A; Cross-references: GB:L14330; GB:L07617; NID:9290210; PIDN:AAB59182.1; PID:9290211

A; Experimental Source: embryo

A; Cross-references: GB:L14320; GB:L07617; NID:9290210; PIDN:AAB59182.1; PID:9290211

A; Experimental Source: embryo

A; Molecule type: mRNA

A; Reference number: A46392

A; MuID:94040709; PMID:1340461

A; Reference number: A46392

A; Reference number: A46392

A; Reference number: A46392

A; Residues: 1350, VV, 352-679, G', 681, L', 683-724, L', 726, H', 728-745, F', 747-911, 'D', 91

A; Cross-references: GB:L05016; NID:9157746; PID:9157747

A; Residues: This protein is required for assembling actin at ring canals in developing eg

C; Comment: This protein is required for assembling actin at ring canals in developing eg

C; Comment: This protein is required for assembling actin at ring canals in developing eg

C; Comment: This protein is required for assembling actin at ring canals in developing eg

C; Comment: This protein is required for assembling actin at ring canals in developing eg

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C; Comment: This protein is required for assembling actin at ring canals in developing eg

C; Comment: This protein is required for assembling actin at ring canals an
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Submitted to the EMBL Data Library, July 1994
A; Reference number: 86565
A; Accession: 86567
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-499 c.TAN>
A; Cross-references: EMBL: D32202; NID: 9927208; PIDN: BAA06901.1; PID: 9927209
B; Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;
A; Title: Cloning, functional expression and tissue distribution of human alpha(IC)-adren
A; Reference number: 865654; MJID: 95255557; PMID: 7737411
                                                                                                                                                                                                                                                                                 adducin homolog - fruit fly (Drosophila melanogaster)
N;Alternate names: D-add; gene hu-li tai shao protein; membrane-cytoskeleton-associated
N;Alternate names: Drosophila melanogaster
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47397; A46332
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A,Cross-references: FlyBase:FBgn0004873
C,Keywords: egg; embryo
                                                                                   FFFLROSFTL-SOAGVAWHDL 22
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A;Residues: 424-499 <hIR>
ZCOSS-references: EMBL:D32202
C;Genetics:
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Cychoches No. 1995.

R.Kohan, R.; Metcalf, M.A.; Khan, N.; Druck, T.; Huebner, K.; Lachowicz, J.E.; Meltzer, J. Neurochem. 66, 47-56, 1996

A.Title: Cloning; characterization, and chromosomal localization of a human 5-HT 6 serott A; Reference number: JC5520; MUID:96102917; PMID:8522988

A.Accession: JC5520

A.Accession: JC5520

A.Residues: 1-440 «KOH»

A.Residues: 1-440 «KOH»

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A.Residues: 1-440 «KOH»

A.Residues: 1-40 «KOH»

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C;Accession: 178885
R;Levedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simmo Oncogene 9, 1977-1888; J194
A;Tile: Two novel human serine/threonine kinases with homologies to the cell cycle regulary A;Reference number: 158396; MUID:94268838; PMID:8208544
A;Reference number: 158396; MUID:94268838; PMID:8208544
A;Reference number: 178885
A;Actus: preliminary; translated from GB/EWBL/DDBJ
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AH2704
methyltransferase Atu1041 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2704
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Best Local Similarity 75.0%; Pred. No. 18;
Matches 15; Conservative 1; Mismatches
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Pred. No. 9.1;
3; Mismatches
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164 LGWHELGHARPPVPGQCRLLAS 185
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R,Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romerov, P.; Zhang, S. Science 284, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: H97486

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-244 «KIR»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biotin synthesis protein bioC VC1114 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: H97486
                                                                                                                                           A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A;Reference maker: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2704
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-244 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42054.1; PID:g17739432; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
A;Genetics: Atul041
A;Map position: circular chromosome
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Pred. No. 6.5;
5; Mismatches
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Pred. No. 6.5;
5; Mismatches
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A.Gene: AGR_C_1920
A.Map position: circular chromosome
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23.4%;
Best Local Similarity 37.1%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
23.4%;
Best Local Similarity 37.1%;
Matches 23; Conservative
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REPEATS.

-!- CAUTION: TIS USED TO SEPARATE THE PRESENCE OF A STOP CODON, *XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
-!- CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino acid sequences.
-!- CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, CDNA libraries also contain partial and/or rearranged CDNAs ligated with Alu-derived sequence in any orientation. Alu-derived sequence in any orientation. Alu-derived sequence in any orientation although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons,
                    homo sapien
gallus gall
mus musculu
felis silve
homo sapien
                                                                                          trypanosoma
haemophilus
                                                                                                           arabidopsis
rattus norv
             rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
Jurka J., Milosavljevic A.;
J. Mol. Svol. 32:105-121(1991).
-!- MOL. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                           Claverie J.-M.; "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
                     P11161
P55879
Q62406
Q9myz3
Q95382
P54258
Q56721
Q57500
                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alu subfamily SX sequence contamination warning entry.
Homo sapiens (Human)
                                                                                                                                                                                                               591 AA
                                                                                                                                                       ALIGNMENTS
                      EGR2_HUMAN
GLI3_CHICK
IRA1_MOUSE
TFR1_FELCA
M3K6_HUMAN
DRPL_RAT
CYA4_TRYBB
Y894_HAEIN
ADRM MOUS
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINES-80201758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
"Alu alert.";
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92241891; PubMed=1572661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
ALU FAMILIES CLASSIFICATION.
MEDLINE=88333009; PubMed=3138422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILIES CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                 Nature 371:752-752(1994).
                                                                                                                                                                                                               STANDARD;
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Quentin Y.;
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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ADRM HUMAN
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J. Mol. Evol. 27:194-202(1988)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 FFETESRSVAQAGVQWRDLGSLQPPPGFKRFSCLSLPSSWDYRRAPPRPANFCIFSRDG 555
consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences being reported.

CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.5%; Score 108; DB 1; 32.2%; Pred. No. 6.1e-06; iive 6; Mismatches 11;
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(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
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FRAME-3.
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FRAME-5.
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MEDLINE=95021758; Pubmed=7935834;
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Mammalia; Eutheria; Primates;
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Matches 28; Conserv
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                                                                 JURKAN J., Milosavijevic A.;
"Reconstruction and analysis of human Alu genes.";
"Reconstruction and analysis of human Alu genes.";
"Mol. 5vol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 CUBRANILISE: THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                being reported.

CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
                                                                                                                                                                                                                                                                                                                                                                                                                  ligated with Aluderived sequence in any orientation. Although Aluelements (especially situated on the complementary strand) have a great potential to create additional/alternative exons. consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
                                                                                                                                                                                                                                                                                                   CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5 or 3 untranslated regions. However, CDNA libraries also contain partial and/or rearranged CDNAs
                                                                                                                                                                                                                       MISCELLANBOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alu subfamily SB2 sequence contamination warning entry.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consequence of erroneous Alu-derived amino acid sequences
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Pred. No. 2.2e-05;
2; Mismatches 5;
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FRAME-2.
FRAME-3.
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FRAME-5.
FRAME-6.
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                                                   MEDLINE=91178815; PubMed=1706781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding nucleotide sequence.
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nilarity 72.4%; Conservative 2,
                                CLASSIFICATION
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196
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593 AA;
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es 21; Conserv
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P39191;
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ALU4_HUMAN
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33

48

Length 603;

39.1%; Score 97; DB 1; 31.2%; Pred. No. 0.00015;

4; Mismatches

Conservative

---DSRASASQSARITGV 48

65272 MW; B8AAD0AD46BEA114 CRC64;

603 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U14570, -; NOT_ANNOTATED_CDS. Hypothetical protein.

1 98 FRAME-
                                       "Alu alert
                                                                        Claverie J
                   SEQUENCE
                                                           CONCEPT
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FRAME-1. FRAME-2. FRAME-3. FRAME-4. FRAME-5.

199 300 401 502 603

102 202 304 405 506

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304 FFLRRSLALSPRPDCGLQWRNLGSLQAPLPGFTPFSCLSLPSSWDYRRPPPRPANFLYFX 363
                                                                                                                                                       4 FFLRQSFTLS---QAGVAWHDLGSLHPPLPGSS-----
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les 29; Conserv
  SEQUENCE
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                                                      Query Match
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Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
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being reported.

CAUTION: Any significant similarity of a putative protein sequence
with an Alu-translated entry must be taken as a warning that a
part of Alu repeat may have been artifactually included in the
coding nucleotide sequence.
                                                                                                                                                                                                                                                                                                 "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, "XXX' IS USED TO SERRAPTE THE VARIOUS TRANSILATION PHASES.
-!- CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                        ALU FAMILIES CLASSIFICATION.
MEDLINE=88333009; Pubmed=3138422;
                                                                                                 MEDLINE=95021758; PubMed=7935834;
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                                                                                                                       Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALU FAMILIES CLASSIFICATION.
                                                                                                                                                                          Nature 371:752-752(1994).
                                                                      FROM N.A.
                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quentin Y.;
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MEDILINE=91178B15; PubMed=1706781;

Jurka J., Milosavljevic A.;

Jurka J., Milosavljevic A.;

"Reconstruction and analysis of human Alu genes.";

J. Mol. Evol. 32:105-121(1991).

-!- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE

THAT ALU REPEATS RALL INTO 8 SUBPAMILIES: THEREPORES, 8 ALU WARNING

CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX

FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: All repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcribts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, cDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu-dements (sepecially situated on the complementary strand) have a great potential to create additional/alternative exons, or some additional/alternative exons, or any oriental and open reading frame may have resulted from a
                                                                                                                                                                                                                                                                                                                                                                                                                  "Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences."; Genomics 12:838-841(1992).
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-!- CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCEI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
                                                                                                   Alu subfamily SP sequence contamination warning entry. Homo sapiens (Human).
                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
  593 AA
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=95021758; PubMed=7935834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALU FAMILIES CLASSIFICATION,
MEDLINE=88333009; PubMed=3138422;
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92241891; PubMed=1572661;
                                                                                                                                                                                                                                                                     Claverie J.-M., Makalowski W.;
"Alu alert.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALU FAMILIES CLASSIFICATION
  STANDARD;
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ALU6 HUMAN
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"Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
Genomics 12:838-841(1992).
cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences
                                                            CAUTION: Any significant similarity of a putative protein seque with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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"The Alu family developed through successive waves of fixation closely connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 96.5; DB 1; Length 593;
Pred. No. 0.00017;
2; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Alu subfamily SB sequence contamination warning entry.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                            136EF344AACD12A2 CRC64;
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MEDLINE=91178815; PubMed=1706781;
Jurka J. Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 FFLRRSFALVAQAGVQWRDLGSPQPPPPG 327
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                                                                                                                                                                                                                                                                                                           FRAME-1.
FRAME-2.
FRAME-3.
FRAME-4.
FRAME-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
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                                                                                                                   coding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            64603 MW;
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Best Local Similarity 69.0°
Matches 20, Conservative
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Nature 371:752-752(1994)
                                                                                                                                                                                                                                                                                                                                                                                                            593 AA;
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                                                 being reportant Augusta
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P39189;
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                                                                                                                                MAI. EVOI. 32:105-121(1991).
MISCELLANGOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                               CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
                                                                            MISCELLANGOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CODON, 'XXX' IS USED TO SEPRANTE THE VARIOUS TRANSLATION PHASES.
CAUTION: This Alu entry is provided in order to avoid the further
poilution of protein sequence databases with Alu-derived amino
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Pred. No. 0.0082;
; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Alu subfamily SB1 sequence contamination warning entry.
Homo sapiens (Human)
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FRAME-4.
FRAME-5.
FRAME-6.
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                                                                                                                                                                                                                                                                                                                                                                             coding nucleotide sequence.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%;
Matches 16; Conservative 4
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296
395
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587 AA;
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P391<u>9</u>0;
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PubMed=7935834;

Claverie J.-M., Makalowski W.;

MEDLINE=95021758;

Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

SEQUENCE FROM N.A. NCBI_TaxID=9606;

01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Alu subfamily SC sequence contamination warning entry.
Homo sapiens (Human).

of fixation

585 AA

STANDARD;

HUMAN

ALUS_HUMAN

4 FFLRQSFTLSQAGVAWHDLGSLHPPLPG 31 493 FFETESRSVAQAGVQWRDLGSLQAPPG

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MEDLINE-91178815; PubMed=1706781;

MEDLINE-91178815; PubMed=1706781;

Jurka J., Milosavljevic A.;

"Reconstruction and analysis of human Alu genes.";

J. Mol. Evol. 32:105-121(1991).

-! MISCELLANDEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE

-! MISCELLANDEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE

THAT ALU REPEATS FALL INTO 8 USERMILIES. THEREFORE, 8 ALU WARNING

CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX

FRANES. CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, CDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a coloning artifact or may be due to mislinterpretation of sequencing that artifact or may be due to mislinterpretation of sequencing that the presence the coloning artifact or may be due to mislinterpretation of sequencing that the coloning artifact or may be due to mislinterpretation of sequencing that the coloning artifact or may be also that the positions, with
                                                                                                              similarity search: alu-derived and other
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                                                                                       Claverie J.-M.;
"Identifying coding exons by similarity sean potentifyly misleading protein sequences.";
Genomics 12:838-841(1992).
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FRAME-2.
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FRAME-5.
FRAME-6.
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                                                                                                                                                              [3]
ALU FAMILIES CLASSIFICATION.
MEDLINE=88333009; PubMed=3138422;
                                                                       MEDLINE=92241891; PubMed=1572661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63573 MW;
 "Alu alert.";
Nature 371:752-752(1994)
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Best Local Similarity
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587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 being reported
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEATS
                                                                                                                                                                                                                     Quentin Y.;
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                                                                                                                                                             CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.
data. This point has been overlooked on several occasions, wit the consequence of erroneous Alu-derived amino acid sequences
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Gaps

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; DB 1; Leus-.

Score 83; DB 1 Pred. No. 0.008 4; Mismatches

33.5%; 57.1%;

4,

Conservative

Length 587;

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-!- MISCELLANDOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBPAMILIES: THEREPORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Additional beguences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain actively transcribed by pol III. Normal transcripts may contain ablu-derived sequences in 5' or 3' untranslated regions. However, CDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (sespecially situated on the complementary strand) have a great potential to create additional/alternative exons. Ornsideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
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CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                  Claverie J.-M.;
"Identifying coding exons by similarity search: alu-derived and other potentially misleading protein sequences.";
genomics 12:838-841(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the consequence of erroneous Alu-derived amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALU FAMILIES CLASSIFICATION.
MEDLINE=91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
"Reconstruction and analysis of human Alu genes.";
                                                                                                                                                                                                           MEDLINE=95021758; PubMed=7935834;
Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88333009; PubMed=3138422;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=92241891; PubMed=1572661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILIES CLASSIFICATION
                                                                                                                                                                                                                                                                   Nature 371:752-752(1994)
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                                                                                                                                                                                                                                                "Alu alert.
                                                                                                                                                                                                                                                                                                             CONCEPT
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RESULT 9
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
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MEDLINE=91178815; PubMed=1706781;

Jurka J., Milosavljevic A.;

Jurka J., Milosavljevic A.;

J. Mol. Evol. 32:105-121(1991).

J. Mol. Evol. 32:105-121(1991).

-! MISCELLANEOUS: VARIOUS ANALYSES (SEE REP. 3 AND REP. 4) INDICATE

THAT ALU REPEATS FALL INTO BUSPAMILIES. THEREFORE, 8 ALU WARNING

CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX

FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANDOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES. CAUTION: This Alu entry is provided in order to avoid the further pollution of protein sequence databases with Alu-derived amino
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Alu family developed through successive waves of fixation closely connected with primate lineage history."; J. Mol. Evol. 27:194-202(1988).
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                                                                                                                                                                                                                                                                                                         46EE8C4F493650A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FFB-1995 (Rel. 31, Created)
01-FFB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0Lu subfamily J sequence contamination warning entry.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 AA.
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                   FRAME-1.
FRAME-2.
FRAME-3.
FRAME-4.
FRAME-5.
                                                                                                                                           EMBL, U14571, -; NOT_ANNOTATED_CDS. Hypothetical protein.

DOMAIN 1 95 FRAME-
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MEDLINE=88333009; Pubmed=3138422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95021758; PubMed=7935834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92241891; PubMed=1572661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 OAGVOWRDLGSLOPPPG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claverie J.-M., Makalowski W.;
                                                                                                                                                                                                                                                                                                           63957 MW;
                                                                                                                                                                                                                                                                                                                                                 31.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
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P39188;
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193
291
489
487
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585 AA;
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                                                                                                                                                                                                                             197
295
393
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SEQUENCE
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Best Local
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acid sequences.

--- CAUTTON: Alu repetitive sequences are interspersed in human and primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcripts may contain Alu-derived sequences in 5' or 3' untranslated regions. However, cDNA libraries also contain partial and/or rearranged cDNAs ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary trand) have a great potential to create additional/alermative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                        being reported. CAUTION: Any significant similarity of a putative protein sequence CAUTION: Any significant similarity of a warning that a with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.
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MEDLINE=98133310; FubMed=9475163;
McNally E.M., Ly C.T., Kunkel L.M.;
McNally E.M., Ly C.T., Kunkel L.M.;
McNally Estion-sarcoglycan is highly related to alpha-sarcoglycan (adhalin), the limb girdle muscular dystrophy 2D gene.";
FEBS Lett. 422:27-32(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76.5; DB 1; Length 591;
Pred. No. 0.054;
4; Mismatches 10; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FFFFLRQSF-TLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665D395735519D95 CRC64;
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28-FEB-2003 (Rel. 41, Last annotation update)
Epsilon-sarcoglycan precursor (Epsilon-SG)
SGCE OR ESG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 AA
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FRAME-2.
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FRAME-4.
FRAME-5.
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Best Local Similarity
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591 AA;
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298
397
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Nigro V.;
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RATAINTENERALENY,

RATAINTENERALELEY,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Is P.W., Hoskins R.A., Galle R.P.,

RA Amanatides P.G., Scherer S.E., Is P.W., Hoskins R.A., Galle R.P.,

RA Mannatides R.A., Lawis S.E., Richards B., Ashburner M., Pfeiffer B.D.,

RA Bradon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Brilew R.M., Basus P.V., Berman J.R., Markers-Fenniscon C.R., Miklos G.L.G.,

RA Ballew R.M., Basus D.W., Berman B.P., Bardario D., Bolashdrov S.,

RA Beron K.Y., Bencos P.V., Berman B.P., Bardario D., Bolashdrov S.,

RA Beron K.Y., Bencos P.V., Berman B.P., Bardario D., Bolashdrov S.,

RA Beron K.J., Evangelista C.C., Fortzez C., Ferriera P., Durn P.,

RA Cherry J.M., Cavley S., Dahlke C., Davenport L.L., Davise P.C.,

RA Choson K., Doup L.E., Downes M., Dugant Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,

RA Glodk A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

RA Glodk A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,

Alali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Linn X.,

RA Mouth S.M., Matteri B., McIntoen T.C., Murshy L., Murshy L., Marsh M., Glasser M.G.,

RA Mount S.M., Moy M., Murphy B., Murshy L., Murshy D.M., Nelson D.L.,

RA Spier E., Spendling A.C., Stunders R.D.C., Scheeler F., Shen H.,

RA Shiers K., Tector C., Turner R., Venter E., Mang X.H., Wang X.H.,

RA Shiers K., Tector C., Turner R., Venter E., Mang X.H., Wang X.,

RA Shiers R., Tector C., Turner R., Venter E., Mang X.H.,

RA Shiers R., Tector C., Turner R., Venter E., Mang X.H., Wang X.H.,

RA Shiers R., Tector C., Turner R., Venter E., Wang X.H.,

RA Shier S., Woodage T., Worley K.C., Wu D., Yung S., Zho O., Zhen J.,

RA Shier S., Woodage T., Worley K.C., Wu D., Yung S., Yao Q., R.

RA Shier S., Rober S.M., Rubin G.M., Venter J.C.,

Ra Shier R., Shone S., Rein-Chall G.M., Weissenbach J.C.,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
                                                                                                                                                                                                                                                                                                                       Yue L., Spradling A.C.; "hu-li tai shao, a gene required for ring canal formation during brosphila shao, encodes a homolog of adducin."; Genes Dev. 6:2443-2454(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
MEDLINE=93211992; PubMed=7681599;
Ding D., Parkhurst S.M., Lipshitz H.D.;
"Different genetic requirements for anterior RNA localization revealed by the distribution of Adducin-like transcripts during Drosophila oogenesis.";
                                                                                                                                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 90:2512-2516(1993)
              16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                                                                                                                                                                                                                     TISSUE=Egg;
MEDLINE=94040709; PubMed=1340461;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:2185-2195(2000).
                                                           Hu-li tai shao protein.
HTS OR CG9325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Berkeley
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                               Ettinger A.J., Feng G., Sanes J.R.;
J. Biol. Chem. 273:19922-19922(1998)
-!- FUNCTION: Component of the sarcoglycan complex, a subcomplex of the dystrophin-glycoprotein complex which forms a link between the F-actin cytoskeleton and the extracellular matrix.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Sarcolemmal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
[3]
SEOURNCE OF 269-413 FROM N.A.
MEDLINE=98070432; PubMed=9405466;
Ettinger A.J., Feng G., Sanes J.R.,
"Epsilon-sarcoglycan, a broadly expressed homologue of the gene mutated in limb-girdle muscular dystrophy 2D.";
J. Biol. Chem. 272:32534-32538(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isoid=043556-2; Sequence=VSP_006018;
-:- TISSUE SPECIFICITY: Ubiquitous.
-:- SIMILARITY: Belongs to the sarcoglycan alpha/epsilon family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
CYS.RICH.
N-LINKED (GLCNAC, . .) (POTEN Missing (in isoform SGCE-2).
/FIIGHVSP_006018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPSILON-SARCOGLYCAN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D87D1899E9C16F23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasma membrane; TAS. complex; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoskeleton; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adhesion; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.11
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 604149; ... cintegral to plasma membri
GO; GO:0005887; Cintegral to plasma membri
GO; GO:0001601; C:sarcoglycan complex; TAS
GO; GO:0007160; P:cell-matrix adhesion; TAS
GO; GO:0007517; P:muscle development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=043556-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF031920; AAC14021.1; ALT_INIT.
EMBL; AF036364; AAC04368.1; -.
EMBL; AJ000534; CAA04167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006644; Cadg.
InterPro; IPR008908; Sarcoglycan_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF05510; sarcoglycan_2; 1.
SMART; SM00736; CADG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
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HTS DROWE
LD THS DROWE
AC 002645; Q9V8U4; Q9V8U5;
DT 01-JUL-1993 (Rel. 26, Created)
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Best Local Similarity 68.47
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                   (Fotential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:10808; SGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Name=SGCE-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=SGCE-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
294
315
211
211
395
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
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RANGE STANDAR SERVICE

DOMAIN

DOMAIN

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SIGNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
      В. Р.
                                                                                                                                                                                                                subfamily.
CAUTION: Ref.3 sequence differs from that shown due to erroneous
                                                      systematic review.";

Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

-!- FUNCTION; Required for assembling actin at ring canals in developing egg chambers. Probably interacts with other developmental proteins involved in nurse cell/occyte transport through the ring canals.

-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                Note=No experimental confirmation available;
DEVELOPMENTAL STAGE: Oogenesis and early embryogenesis.
MISCELLANEOUS: 'Hu-li tai shao' means 'too little nursing' in
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.,
                                                                                                                                                                                                     SIMILARITY: Belongs to the aldolase class II family. Adducin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                   "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; 5AA90E8938A84A0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
                                                                                                                                                         IsoId=Q02645-2; Sequence=VSP_000191, VSP_000192;
                                                                                                                     Event=Alternative splicing; Named isoforms=2; Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 1
Pred. No. 1.8;
5; Mismatches
                                                                                                                                        IsoId=002645-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                     EMBL; D0S016; AAA28643.1; -.
EMBL; AF151708; AAB5182.1; -.
EMBL; AE003796; AAF57565.3; ALT SEQ.
EMBL; AE003796; AAF57566.2; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127938
                                                                                                                                                                                                                                 gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                  EMBL, AE003796, AAF
PIR, A47397, A47397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
680
689
725
746
912
1089
                                                                                                                                                   Name=Short,
                                                                                                                                                                                               Chinese.
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ò g 11 RESULT

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PRT; 741 AA.

FREDI HUMAN STANDARD; PRT; 741 AA.

P78553; 000395; 000465; 000691; 000692; P78555;
01-NOV-1997 (Rel. 35, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Double-stranded RNA-specific editase 1 (EC 3.5...) (dsRNA adenosine deaminase) (RNA editing deaminase 1) (RNA editing enzyme 1).

ADAREL OR REDI OR DRADA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;

Event=Additional isoforms seem to exist;

Name=1; Synonyms=RED1-L, DRADA2B;

IsoId=P78563-1; Sequence=Displayed;

Name=2; Synonyms=RED1-S, DRADAAA;

IsoId=P78563-2; Sequence=VSP_000865;

Name=2; Synonyms=DRADA2C;

IsoId=P78563-3; Sequence=VSP_000866;

IsoId=P78563-3; Sequence=VSP_000866;

IsoId=P78563-3; Sequence=VSP_000866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97265373; PubMed=9111310;
Lai F., Chen C.-X., Carter K.C., Nishikura K.;
"Editing of glutamate receptor B subunit ion channel RNAs by four
alternatively spliced DRADA2 double-stranded RNA adenosine
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Fetal brain;
MEDLINE=97288518; PubMed=9143496;
MEDLINE=97288518; PubMed=9143496;
Mittaz L., Scott H.S., Rossier C., Seeburg P.H., Higuchi M.,
Antonarakis S.E.;
Antonarakis S.E.;
"Cloning of a human RNA editing deaminase (ADARBI) of glutamate
receptors that maps to chromosome 21q22.3.";
Genomics 41:310-217(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
MEDLINE=97471700; PubMed=9330641;
Villard L., Tassone F., Haymowicz M., Welborn R., Gardiner K.,
"Map location, genomic organization and expression patterns of
human RED1 RNA editase.",
Somat. Cell Mol. Genet. 23:135-145(1997).
                                                                                                                                                                                                                                                                                                                                                                                                   Gerber A., O'Connell M.A., Keller W.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 17:2413-2424(1997)
                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deaminases.
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REDINE=21638749; PubMed=11780052;

REDINE=21638749; PubMed=11780052;

REDINE=21638749; PubMed=11780052;

REDINE=21638749; PubMed=11780052;

REDINE=21638749; PubMed=11780052;

REDINE=21638749; PubMed=1780052;

REDINE=21638749; PubMed=1780052;

REDINESTED REDINE R. Blakey S.E., Bridgeman A.K., Barown A.G., Basiley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.G., RA Buck D., Buller A.P., Carder C., Carter D.P., Carter D.P., Carter D.P., RA Buck D., Buller R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garrer P., RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Halley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Ramberley A.M., King A., Knights A., Laird G.K., Lowlor S., Holden J.L., Howden P.D., RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Ray M.P., Mistry D., McCre M.J.F., Mullikin J.C., Nickerson T., M. Milne S.A., Mistry D., McCre M.J.F., Mullikin J.C., Nickerson T., RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Ross M.T., Scott C.E., Schra H.K., Shownkeen R., Sins S., Sawan R.M., Sycamore N., Taylor R., Tee, J. Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Walliams L., Williams S.A., Wilhielped S.L., Whittaker P., Williey D.L., Williey D.L., Williams E., Williams S.A., Ranche D.W., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Williey D.L., Williams E., Williams E., Williams D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche D.M., Ranche 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insoid=Q8TDM0-2; Sequence=VSP_007854, VSP_007855, TISSUE SPECIFICITY: Brain, thymus, spleen, kidney and placenta. Overexpressed in most breast cancer cell lines. DISBASE: May be involved in breast cancer through a t(17,20) (q23;q13) chromosomal translocation that involves BCAS3
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND CHROMOSOMAL TRANSLOCATION WITH BCAS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 14-211 FROM N.A. (ISOFORM 1).
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human con'A sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                            MEDLINE=22265331; PubMed=12378525;
Baerlund M., Monni O., Weaver J.D., Kauraniemi P., Sauter G., Heiskanen M., Kallioniemi O.-P., Kallioniemi A.;
"Cloning of BGAS3 (17q23) and BCAS4 (20q13) genes that undergo amplification, overexpression, and fusion in breast cancer.";
Genes Chromosomes Cancer 35:311-317(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the cappuccino family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 27-211 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isold=Q8TDM0-1; Sequence=Displayed;
                                         wammalia; Euther:
NCBI_TaxID=9606;
                                                                                                                                                                                                    TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
SIMILARITY: Contains 2 DRBM (double-stranded RNA-binding) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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DRBM 2.

ZINC 8. SIMILARITY).

BY SIMILARITY.

ZINC (BY SIMILARITY).

MISSING (BY SIMILARITY).

MISSING (BY SIMILARITY).

MISSING (BY SIMILARITY).

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MISSING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 601218; -.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0004000; F:adenosine deaminase activity; TAS.
GO; GO:0003725; F:double-stranded RNA binding; TAS.
GO; GO:0007417; P:central nervous system development; TAS.
GO; GO:0006396; P:RNA processing; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65.5; DB 1; Length 7 Pred. No. 1.7; 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 LEGSRSYTQAGVQWCNHGSLQPRPPGLLSDPSTSTFQGAGTT 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002466; A deamin.
InterPro; IPR00159; DS RBD.
Pfam; PF001137; A deamin; 1.
Pfam; PF001317; A deamin; 1.
SWART; SM00552; ADEAM; 2.
SWART; SM00558; DSRM; 2.
PROSITE; PS50141; A DEAMIN EDITASE; 1.
PROSITE; PS50137; DS RBD; 2.
PROSITE; PS50137; DS RBD; 2.
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02B583414DD59C20 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G -> A (IN REF. 4).

R -> E (IN REF. 4).

V -> L (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoform 3)
/FTId=VSP
                                                                                                                                                                                                                                                                                                               EMBL; U82120; AAB61686.1; EMBL; U92121; AAB61687.1; EMBL; V99227; CAA67611.1; EMBL; V99383; CAA67762.1; EMBL; U76420; AAC51240.1; EMBL; U76420; AAC51240.1; EMBL; U76422; AAC51241.1; EMBL; U76422; AAC51241.1; EMBL; U76422; AAC51241.1; EMBL; AF001042; AA583300.1; EMBL; AL163301; CAB90493.1; EMBL; AL163301; CAB90493.1; Genew; HGNC:226; ADARB1. GK; P78853; CAB7801.1; CAB7801.1; CAB78853; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1; CAB7801.1
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1 Similarity 45.2%;
19; Conservative 3
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423
475
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423
475
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396
4551
466
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DOMAIN 76
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METAL
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CONFLICT
CONFLICT
SEQUENCE
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BCAS4. Homo sapiens (Human).

DE DE DE OS

Query Match

Best Loca Matches

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RESULT 12 BCS4 HUMAN

VARSPLIC VARSPLIC

DOMAIN

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   and for commercial
                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                 -> KSPAPVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOIG-014628-3; Sequence-Not described;
ISSUE SPECIFICITY: EXPRESSED IN ADULT HEART, BEAIN, PLACENTA,
TISSUE SPECIFICITY: EXPRESSED IN ADULT HEART, KIDNEY AND BRAIN.
STRELFTAL MUSCLE, AND PANCREAS, AND IN PETAL LUNG, KIDNEY AND BRAIN.
THERE IS LITTLE EXPRESSION IN ADULT LUNG, LIVER AND KIDNEY.
SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C242-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=9806942; PubMed=9944677;
Hussey D.J., Parker N.J., Hussey N.D., Little P.F.R., Dobrovic A.;
"Characterization of a KRAB family zinc finger gene, ZNF195, mapping
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                              TYELPTLYRTEDYFPVDAGEA (in isoform 2)
/FIId=VSP 007854.
Missing (In isoform 2).
/FIId=VSP 007855.
E -> D (in dbSNP:272962).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     BREAKPOINT FOR TRANSLOCATION TO FORM
                                                                                                                                                                                     Alternative splicing; Proto-oncogene; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                   BCAS4-BCAS3.
AFVKMVGHHVAFLEADVLQAERDHGAFPQ
                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
   Usage by
                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_016031.
D16930DBC982AF5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
ZNF195 OR ZNFP104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to chromosome band 11p15.5.";
Genomics 45.451 455 (1997).
--- SUBCELLULAR LOCATION: Nuclear (Probable).
--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                  IsoId=014628-2; Sequence=Not described;
modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=014628-1; Sequence=Displayed;
Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 KRAB domain.
                                                            EMBL, AF361220, AAL99633.1; -
EMBL, AF361221, AAL99633.1; -
EMBL, AL01680, CAB44746.2; -
EMBL, AL13328, CAB37375.1; -
EMBL, AK000502, BAA91209.1; AIT INIT.
EMBL, AK000502, BAA91209.1; AIT INIT.
Genew, HGNC:14367; BCA84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 LPGSSDSPASASQVAGITEV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 LPGSSDSRASASQSARITGV 48
                                                                                                                                                                                                                                                                                                                                                             22758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                      61
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                             211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                148
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                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                         Polymorphism.
                                                                                                                                                                        MIM; 607471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z195 HUMAN
O14628;
                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                               VARIANT
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Z195 HUMAN
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for commercial
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TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=96421968; PubMed=8824585; Hu M.C.-T., Qiu W.R., Wang X., Meyer C.F., Tan T.-H.; Hu M.C.-T., Qiu W.R., Wang X., Meyer C.F., Tan T.-H.; In a movel human hematopoietic progenitor kinase that activates the JNK/SAPK kinase cascade."; Genes Dev. 10:2251-2264 (1996).

-!- FUNCTION: May play a role in the response to environmental stress. Appears to act upstream of the c-jun N-terminal pathway.
                                                                                                                                                                                                                                                      R MING BOLZEST, C: mucleus; NAS.
R GO: GO:0005634; C:nucleus; NAS.
R GO: GO:0005634; C:nucleus; NAS.
R GO: GO:0005637; F:DNA binding; NAS.
R GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
R R GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
R INTERPRO; IPR001909; KRAB.
R INTERPRO; IPR001909; KRAB.
R Ffam; PF01352; KRAB.
R Ffam; PF01352; KRAB.
R Ffam; PF01352; KRAB.
R FACTIST: SM00349; KRAB.
R SWART; SM0035; ZIF C2H2; 9.
R RRART; SM00355; ZIF C2H2; 9.
R ROSITE; PS0605; KRAB; 1.
R RROSITE; PS06028; ZINC_FINGER_C2H2 2; 10.
R Zinc_finger; Metal-binding; DNA-binding; Nuclear protein;
A literative splitcing.
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(MEKKK 1)
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ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
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ID M4K1 HUMAN

M2 092918;

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last sequence in (EC DE Mitogen-activated protein kinase kinase i) (MEY (MARK/ERK kinase kinase i) (MEY (MARK/ERK kinase kinase i) (MEY Homse kinase i) (MEY Homse kinase i) (MEY Homse kinase i) (MEY Homse kinase i) (MEY Homse kinase i) (MEY Homse kinase i) (MEY Homse kinase i) (MEY Homse ii)
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2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRAB.
SPACER.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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HSSP; P08046; lAlG.
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Matches 16, Conservative
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629 AA;
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ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
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                   NCBI_TaxID=10784;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 -!- FUNCTION: May play a role in hematopoietic lineage decisions and growth regulation (By similarity).
-!- CATALYTICA CATIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- COFACTOR: Magnesium.
-!- SUBUNIT: Interacts with MAADSKI.
-!- TISSUE SPECIFICITY: Expressed primarily in hematopoietic organs, including bone marrow, spleen and thymus. Also expressed at very low levels in lung, kidney, mammary glands and small
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Pfam; PFOOT080; CM1; 1.
Pfam; PFOOT080; CM1; 1.
PRINTS; PROOT009; TYRKINASE
PRODOM; PDOOT001; Proc_Kinase; 1.
SMART; SMO0220; CM1; 1.
PROSITE; SMO010; PROTEIN KINASE ATP; 1.
PROSITE; PSO0101; PROTEIN KINASE DOM; 1.
PROSITE; PSO0108; PROTEIN KINASE DOM; 1.
PROSITE; PSO0108; PROTEIN KINASE ST; FALSE NEG.
ATP-binding; Transferse; Kinase; Serine/threonine-protein kinase.
                                                                                                                                                                                                                                                                                                                                                              R MIM; 601983; ---

R GO; GO:000524; F:ATP binding; IDA.

GO; GO:000524; F:ATP binding; IDA.

GO; GO:0007257; P:protein serine/threonine kinase activity; IDA.

GO; GO:0007257; P:protein dino acid phosphorylation; IDA.

GO; GO:0007243; P:protein amino acid phosphorylation; IDA.

GO; GO:0007243; P:protein amino acid phosphorylation; IDA.

GO; GO:0007243; P:protein kinase cascade; IDA.

R GO; GO:0005850; P:response to stress; IDA.

InterPro; IPR000719; Prot. kinase.

R InterPro; IPR0019; Prot. kinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                    SIMILARITY: Belongs to the Ser/Thr family of protein kinases. STE20 subfamily.
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Pred. No. 5.3;
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3C98CF01BE42E151 CRC64;
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01-APR-1988 (Rel. 07, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Noncapsid protein NS-1 (Nonstructural protein NS1).
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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833 AA; 91296 MW;
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ilarity 53.3%;
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Genew; HGNC:6863; MAP4K1.
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                                                                                              "Complete nuclectide sequence and genome organization of bovine
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                 MEDLINE-87061184; PubMed=3783814;
Chen K.C., Shull B.C., Moses E.A., Lederman M., Stout E.R.,
Bates R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, M14363; AAB59845.1; -PIR, C26104; UYPVS1. Parvo NS1. Fam, PF01057; Parvo NS1. Nonstructural protein; Noncapsid protein; DNA replication; ATP-binding.
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42659A611A3AF038 CRC64;
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30.0%; Pred. No. 6;
iive 6; Mismatches
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T Virol. 60:1085-1097(1986)
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Q8N4K1 Q8N8F4 Q9UHT1 Q9HA45 Q9HA67 Q9HA67

Q96HX1 O75228 Q8TB48 Q9UCY2

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ALIGNMENTS

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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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No.
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homo sapien homo sapien homo sapien macaca fasc homo sapien

Q96ebl h Q9b5d5 h Q9ui48 h Q95kel m

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EMBL; AB055293; BAB21918.1; -. Hypothetical protein. SEQUENCE 122 AA; 13539 MW;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.73
Matches 23; Conservative
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                                                     SEQUENCE
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                                                                                                                                                                                  SECUENCE FROM N.A.
Shichilo S., Itoh K.;
Shichilo S., Itoh K.;
"Identification of immuno-peptidmics that recognized by tumor-reactive
CTL generated from TIL of colon cancer patients.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062477; BAB93502.1;
SEQUENCE 109 AA; 11580 MW; FBS200153CEE2B33 CRC64;
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TISSUB-ILEAL MUCOSA;
Watanabe K., Kumagan A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
NEDO human CDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00385; BAA91131.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
Hypothetical protein FLJ20837
Hymochetical protein FLJ20837
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidee, Homo.
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
OK/SW-CL.41.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 54.4%; Score 135; DB 4; Length 10 Best Local Similarity 65.9%; Pred. No. 4.1e-10; Matches 27; Conservative 6; Mismatches 9; Indels
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SEQUENCE 152 AA; 16568 MW; 59065F45AAA301B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESHSVTQAGVQWHDLGSLHSPLLGSSDSPTSASRVAGITGM 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV 48
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FL720378.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 DMGFPHVGQTGLELLTSGDPPASASQSAGITG 114
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01-OCT-2000 (
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Matches
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Q9NX85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Frontal.cortex;
Osada N., Hida M., Xusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ39655.
Hypothetical protein FLJ39655.
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; NBDO human cDNA sequencing project.", Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

BMBL, AKO00844, BAA91396.1; -. SEQUENCE 208 AA; 23290 MW; C916648B9CAE4520 CRC64;
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
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                                                                                                                                                                                                                                                                                                  Length 208;
                                                                                                                                                                                                                                                                                              50.0%; Score 124; DB 4; Length 20
65.7%; Pred. No. 2.5e-08;
.ive 5; Mismatches 7; Indels
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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NCBI_TaxID=9606;
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01-OCT-2002
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Q8N874;
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"NEDO human cDNA sequencing project.";
BMBL, AK092844: BAC03988.1;
                 TISSUE-BRILL intestine;

Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,

Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,

Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,

Ctsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma Matsuo K., Nagahari K., Sekine M., Kikuchi H., Kanda K., Wagatsuma P., Sugano S., Magahari K., Masuho Y., Magai K., Isogai T.;

Supano S., Magahari K., Masuho Y., Magai K., Isogai T.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO96974; BAC04918.1;

Hypothetical protein.

SEQUENCE 121 AA, 12917 MW, 4026598DE8735432 CRC64;
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QBNAL9;
QBNAL9;
Q1-OCT-2002 (TTEMBLrel. 22, Last sequence update)
O1-OCT-2002 (TTEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ35131.
Hypothetical protein FLJ35131.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FL/35525.
Hypothetical protein FL/35525.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                    Length 121;
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Pred. No. 4.6e-08;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FFFFTLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITG
                                                                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            3 FFFLROSFILSOAGVAWHDLGSLHPPLPGSSDSRASASOSARITGV
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162 AA; 17880 MW; E6D94CE17D0DCC71 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Score 122; DB 4;
Pred. No. 2.4e-08;
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56.5%;
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Best Local (
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Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,
Xu W., Gao F., Liu M., He F.;
"Functional prediction of the coding sequences of 75 new genes deduced
by analysis of cDNA clones from human fetal liver.";
Submitted (FRE-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF130089, AAG35515.1;
SEQUENCE 118 AA, 13257 MW; 94688870CAC8760D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFFLFLRWSFTLVAQAGVQWRDLSSPQPPPPRFKRFSCLSPPSSWDYRHAPPHPANFVFL
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Minomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Puruya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanihashi M., Yamazaki M., Sugiyama T., Irie R., Ocsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai Hio Y., Satio K., Nishikawa T., Kimura K., Yamashita H., Kanehori K., Nakamira Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B. Suzuki Y., Sugano S., Nagahari K., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

RMBI, AKO92450; BACO33931; -.

RMBI, AKO92450; BACO33931; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
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Last sequence update)
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Pred. No. 1.1e-07;
5; Mismatches 11
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33.0%;
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16,
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.0°
Matches 31; Conservative
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Last annotation update)

us-10-082-830-224.rspt

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es 19; Conserv
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                                                                                           Q96EB1;
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                                                                      Q96EB:
                           RESULT 12
Q96EB1
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                                                                                                                                                                                         Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Saro H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Madtsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
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                                                                Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK097342; BAC05007.1; -.
Hypothetical protein.
SEQUENCE 157 AA; 17930 MW; D79F77F33B7C608E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
43.8%; Score 108.5; DB 4.
Best Local Similarity 34.1%; Pred. No. 1.8e-06;
Matches 31; Conservative 4; Mismatches 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
01-OCT-2002 (TrEMBLrel, 22, La Hypothetical protein FLJ39895. Homo sapiens (Human),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein FLJ40023.
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nes 19; Conservative
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                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                           TISSUE=Spleen;
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Q8N845;
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Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Kawakami T., Noguchi S., Itoh T., Snigami A., Fujiwara T., Ono T.,
Yamada K., Fujii Y., Ozaki K., Hirao M., Omnori Y., Ota T.,
Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
Isogai T., Sugano S.,
Insogh Man cDNA sequencing project.";
Submitted (AuG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK027208; BAB15692.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryoča, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.5%; Score 105.5; DB 4; Lengua. 57.8%; Pred. No. 2.1e-05; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 FFFLROSFILSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012114; AAH12514.1; -.
Genew, HGNC11171; ELP4.
InterPro; IRF008728; PAXNEB.
Pfam; PF05625; PAXNEB.
Pfam; PF05625; PAXNEB; 1.
SEQUENCE S35 AA; 58713 MW; 86E6DD3B545E96D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AA; 17632 MW; C9A857907E44D2E8 CRC64;
                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.3%; Score 105; DB 4; Lilarity 61.3%; Pred. No. 6.1e-06; Conservative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 FFFFFEMESCSVPHAGVQWHDLGSQQPPPPG 139
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Testis, and Embryonic carcinoma;
                                                19, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRT;
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Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                              01-DEC-2001 (TrEMBLrel.
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EQUENCE FROM N.A.

TISSUE-Frontal Cottex;

Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

Suzuki Y., Sugano S., Hashimoto K.;

Libraries. "Isolation of full-length cDNa clones from macaque brain cDNa "

Inbraries.", Submitted (UUN-2001) to the EWBL/GenBank/DDBJ databases.

EMBL, AB062994; BAB60728.1; --

EMBL, AB062994; BAB60728.1; --

EMBL, AB062994; BAB60728.1; --

EMBL, AB062994; BAB60728.1; --

EMBL, AB062994; BAB60728.1; --

EMBL, AB062994; BAB60728.1; --

EMBL, AB062994; BAB60728.1; --

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                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
Yu Y., Zhang C., Luo L., Ouyang S., Zhang S., Li W., Wu J., Zhou S.,
Liu M., He F.;
Liu M., He F.;
Liu M., He F.;
Functional prediction of the coding sequences of 50 new genes deduced
by analysis of cDNA clones from human fetal liver.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF090944; AAF4056.1;
SEQÜENCE 61 AA; 7364 NW; AAFE987A88277368 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryca, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithezinae; Macaca.
                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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41.3%; Score 102.5; DB 6; Length 135;
Best Local Similarity 48.9%; Pred. No. 1.1e-05;
Matches 23; Conservative 3; Mismatches 10; Indels 11;
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Pred. No. 3.7e-06;
3; Mismatches 9; Indels
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) PR00663 (Fragment).
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Best Local Similarity 61.3%;
Matches 19; Conservative
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August 10, 2004, 19:10:16; Search time 54 Seconds (without alignments) 251.153 Million cell updates/sec
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1 FFFFLRQSFTLSQAGVAWH.....LPGSSDSRASASQSARITGV 48
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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seg length: 200000000
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Maximum DB
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A_Geneseq_29Jan04:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human sec Neural th Novel hum HLA-B46 T Human | Novel | Human Human Novel Human Novel Human Novel Human Human Novel Human Human Novel Novel Novel Description Adc87115 1 Adc87151 1 Aau32787 Aau32786 Aam25539 Aac11780 Adc86929 Aau31783 | Adb64520 | Abg10943 | Abq65595 Aau31652 Aau29593 Aau30350 Abp55149 Add22434 SUMMARIES AAU31783 ADB64520 AAU31552 AAU32788 AAU30350 **ABP55149** Query Match Length DB 100 100.0 248 160 160 159.5 153 152 1447 1444 1440 1380 1370 1370 1370 Score Result

71 4 AAU33302 116 4 AAU33214 116 4 AAU32314 116 4 AAU32072 229 4 AAU30354 53 4 AA010596 67 4 AA010596 70 4 AA010596 101 4 AA032073 103 4 AAU33189 104 4 AAU33189 104 4 AAU33281 107 7 ADD19226 117 7 ADD19226 118 4 AAU32881 117 7 ADD192282 118 4 AAU32881 118 4 AAU32881	Aau33302 Novel hum	Aau33214 Novel hum	Novel	Adb37629 Neural th	Aau32072 Novel hum	Novel	Aaol0159 Human pol	Human	Aao10596 Human pol	Aao02241 Human pol	Aau32073 Novel hum	Aao08294 Human pol	Aau33189 Novel hum	Aau33156 Novel hum	Aau33281 Novel hum	Aao10724 Human pol	Add19326 Human sec	Add19292 Human sec	Aau32881 Novel hum	Aau29573 Novel hum	
44474444444444	AAU33302	AAU33214	AAU14736	ADB37629	AAU32072	AAU30354	AA010159	AAM95665	AA010596	AA002241	AAU32073	AA008294	AAU33189	AAU33156	AAU33281	AA010724	ADD19326	ADD19292	AAU32881	AAU29573	
	71 4	11 4	9	7 2	4 4	4	3 4	8 4	7 4	70 4	1 4	3 4	4 4	4 4	4 4	17 4	7 7	7 7	8 4	4 4	
	53.0	53.0	53.0	52.8	52.8	52.8	52.4	52.4	52.4	52.4	52.4	52.4	52.2	52.2	52.2	52.0	52.0	52.0	52.0	51.8	
0.000 0.000	131.5	131.5	131.5	131	131	131	130	130	130	130	130	130	129.5	129.5	129.5	129	129	129	129	128.5	
www.dddooooowwwwwwww.	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

Human, breast specific protein, BSP, breast cancer, vaccine, mammary tumour, cytostatic, gene therapy, non-cancerous breast disorder. Human breast specific polypeptide, BSP #65. ABG65595 standard; protein; 48 AA. (first entry) 23-AUG-2002 ABG65595; ABG65595

29-OCT-2001; 2001WO-US046888 WO200236807-A2 Homo sapiens. 10-MAY-2002.

Turner LR; Liu C, Salceda S, 27-OCT-2000; 2000US-0243802P (DIAD-) DIADEXUS INC. Recipon H, Sun Y,

New breast-specific nucleic acids and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissues. WPI; 2002-463415/49.

GPC GPC hum hum Claim 11; Page 245; 281pp; English.

The invention relates to breast specific nucleic acids (BSNA) and breast-specific polypeptides (BSP). Also included are a method for determining the BSNA in a sample, a vector comprising a BSNA, a host cell comprising the vector, a method for producing a polypeptide encoded by a BSNA, an anti-BSP antibody and a method for determining the presence of a BSP in a sample. The breast-specific mucleic acids, polypeptides and compositions comprising them are useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer, mammary tumour and non-cancerous disease states in breast tissue; for identifying breast tissue; for monitoring, identifying and/or designing agonists and antegonists of the polypeptides; in gene therapy; in producing transgenic animals and cells; for producing engineered breast tissue for treatment and research, and as elements in an array or computer program for pattern recognition

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Human

AAU71968

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Gaps

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11; Indels

Length 110;

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the cucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of the action and therapy, and can be used as untitional supplements. They may be used to increase stem cell proliferation, to requirate haematopoissis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. Secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation; haematopoiesis, nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                 1 FFFFEMESRIVIQAGVQWHDLGSLQPPPGSSDSPVSASHVAEITG 46
                                                                                                                               2 FFFFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITG 47
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/ Match
Local Similarity 69.6%; Pred. No. 3.7e-13;
les 32; Conservative 5; Mismatches 9; Indels
                      Score 160; DB 4;
Pred. No. 3.6e-13;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 663-664; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted protein #3279.
                                                                                                                                                                                                                                                                                                                   AAU32788 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6-APR-2001; 2001WO-US008656.
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26-JAN-2001; 2001US-00770160.
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                           64.5%;
69.6%;
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                                                                                Conservative
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                           Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200179449-A2.
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Matches
                                                                                                                                                                                                                                                                 RESULT 3
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of breast disorders. The nucleic acids may be used as hybridisation probes to detect, characterise and quantify hybridising nucleic acids in, and isolate hybridising nucleic acids from, both genomic and transcripterived nucleic acid samples. The BSP protein may be used in a vaccine composition for raising an immune response against breast cancer. The present sequence is BSP protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
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                                                                                                                                                                                                                                                                                                                                           48
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                                                                                                                                                                                                                                                                                       Indels
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0
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Pred. No. 3.4e-25;
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #2043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU31552 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 457; 765pp; English.
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                 Local Similarity 100.
ses 48, Conservative
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                                                                                                                                                                                      Sequence 48 AA;
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25-0CT-2001

Tang YT,

18-DEC-2001

AAU31552;

RESULT 2 AAU31552

Query Match

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Gaps

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31 FFFFETESCSVAQAGVQWHDLGSLQPPPPGSSDSPASASRVAGIIG 76

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Sequence 110 AA;

Length 113;

AA.

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human; GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                          NAT INST ADVANCED IND SCI & TECHNOLOGY.
CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                             Human GPCR protein SEQ ID NO:1568.
ADC87115 standard; protein; 176
                                                                                                                                                                                                                         18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                 18-JUN-2001; 2001JP-00246789
                                                                                                                                                                                                                                                                                                                                           WPI; 2003-315783/31.
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                                                                                                                                              Homo sapiens.
                                                                                                                                                                    EP1270724-A2.
                                                                                                                    gene therapy
                                                   01-JAN-2004
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                                                                                                                                                                                                                                                                                                                Suwa M,
                                                                                                                                                                                                                                                                                         (ADSC-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at herapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stam cell proliferation, to regulate haematopoissis, and in bone, cartiage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammantory agents; and in treatment of leukaemias. Autusbato-the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                     Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SSDSRASASQSARITGV
                                                 AAU31652 standard; protein; 105 AA.
                                                                                                                              Novel human secreted protein #2143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 492; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                               Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                      16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                              2000US-00552929
2001US-00770160
                                                                                                     (first entry)
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es 38; Conserv
                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105 AA;
                                                                                                                                                                                                                                WO200179449-A2
                                                                                                                                                                                                           Homo sapiens,
                                                                                                                                                                                                                                                                                                              18-APR-2000;
26-JAN-2001;
                                                                                                     18-DEC-2001
                                                                                                                                                                                                                                                          25-OCT-2001
                                                                          AAU31652;
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                                     AAU31652
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Aburatani H;

Asai K, Akiyama Y,

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                                                                                                                                                                                                           The invention relates to a novel polynucleotide encoding a guanosine triphosphare-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide of polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the quanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; GPCR; guanosine triphosphate-binding protein coupled receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.7%; Score 153; DB 7;
66.0%; Pred. No. 5.1e-12;
iive 4; Mismatches 12,
                                                                                                                                            Claim 2; SEQ ID NO 1568; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GPCR protein SEQ ID NO:1604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 176 AA;
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RESULT 5 ADC87115

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(NAAD-) (ADSC-)

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition of disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a pents of the proteins are useful for identifying a percent of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acide encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used a suntitional supplements. They may be used to increase stem cell proliferation; to regulate haematorpoiseis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias.

Al129510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.3%; Score 152; DB 4; Length 114; 66.7%; Pred. No. 4.3e-12; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFFFFTTSHCVAQAGVQWLDLGSLQPPPGSSNSPASASQVAGTTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FFFFFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU29593 standard; protein; 85 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2001; 2001WO-US008656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a vaccination, testing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU29593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel polynuclectide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the quanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                                                           New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.7%; Score 153; DB 7; Length 217; 68.1%; Pred. No. 6.5e-12; ive 4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FFFFFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITG 47
                                                                                                              & TECHNOLOGY.
                                                                                                                                                                                    Akiyama Y, Aburatani H;
                                                                                                              NAT INST ADVANCED IND SCI & TEC
CENT ADVANCED SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 1604; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted protein #3278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU32787 standard; protein; 114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT;
                  18-JUN-2002; 2002EP-00013517.
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2001US-00770160.
                                                                18-JUN-2001; 2001JP-00246789
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                                                                                                                                                                                                                                     WPI, 2003-315783/31.
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nes 32; Conserv
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                                                                                                                                                                                    Suwa M, Asai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Liu C,
                                                                                                                                                                                                                                                               N-PSDB; ADC87150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200179449-A2.
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26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Query Match

Best Loc Matches

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Gaps

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            to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem call proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU20510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidecterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
  nucleic acids encoding the polypeptides and cells genetically engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the human secreted proteins AAB28012-B28060. This sequence represents a peptide fragment homologous to the protein encoded by the gene given in the descriptor line. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to the isolation of genes AAC59108-C59156 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammatory disorders,
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein BLAST search protein SEQ ID NO: 109.
                                                                                                                                                                                                                                                                                                              1 FFFFFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
                                                                                                                                                                                                                                                                                                                                  14; Indels
                                                                                                                                                                                                                                  Score 147; DB 4; Length
Pred. No. 1.4e-11;
4; Mismatchès 14; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating cancers, hyperproliferative disorders, inflaneurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 364-365; 389pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB28061 standard; protein; 70 AA
                                                                                                                                                                                                                                59.3%;
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99US-0168654P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2000; 2000WO-US006058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                  Local Similarity 62.5
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-638177/61
                                                                                                                                                                                             85 AA;
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Matches
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The present invention relates to AD7c-neural thread protein (NTP) and related proteins and peptides (I; ADB37528-ADB37641). The sequences are useful for treating a condition in a patient requiring removal or destruction of cells. The condition can be selected from benign or inalignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a tissue, virally, bacterially or parasitically altered tissue, or malformation of a tissue, where the tissue is selected from Lung, breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus, colon, intestine, stomach, rectum, ossophagus, heart, splen, salivary gland, blood, brain and its coverings, spinal cord and its coverings, muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary, reproductive organs, liver, gall bladder, eye, ear, nose, throat, consils, mouth, lymph nodes and lymphoid tissue. The condition is preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis, ceream, dermatosis, commetic modification to a tissue (skin, eye, ear, nose, throat, mouth, muscle, connective, hair or breast tissue), vascular disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiatherosclerotic, Antiarteriosclerotic; Vasotropic; Antiinflammatory, Immunosuppressive, Tranquillizer, Antiemetic, Virucide, AD7c-NTP, neural thread protein; neuritic sprouting.
                  arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischamias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parastit infections
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Related peptide or AD7c-neural thread peptide, useful for tr
unwanted cellular proliferations, glandular hyperplasia, unwanted
hair, warts and unwanted fatty tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for
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                                                                                                                                                     Score 144; DB 3; Length 70;
Pred. No. 2.8e-11;
7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                          PFFFFFFTESCSVAEAGVQWCDLGSLKSPPPGSSDSPASASRVAGITGM
                                                                                                                                                                                                                                      FFFFFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
    multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; Antitumour; Antipsoriatic; Dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neural thread protein-related protein #63.
  diabetes mellitus, Crohn's disease,
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                                                                                                                                                                                                                                                                                                                                                                           ADB37600 standard; protein; 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001; 2001US-0306150P.
19-JUL-2001; 2001US-0306161P.
16-NOV-2001; 2001US-0331477P.
                                                                                                                                                         58.1%;
62.5%;
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                                                                                                                                                                                               30; Conservative
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                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                    70 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified,
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ADB37600
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                                                         fibrosis disease, storage disease, congenital malformation, enzyme deficiency disease, potential, intoxication, environmental disease, radiation disease, potential disease, and disease, endocrine disease, degenerative disease and mechanical disease. The peptides are useful for treating unwanted cellular probliferations, glandular (e.g. prostate) hyperplasia, unwanted facial hair, warts and unwanted fatty tissue, or for preparing antibodies that recognize and/or bind to Related proteins, Related peptides or NTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                    Gaps
veins, inflammatory disease, autoimmune disease, metabolic disease, hereditary/genetic disease, traumatic disease or physical injury, nutritional deficiency disease, infectious disease, amyloid disease,
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                                      2 FFFFFETESCSVAEAGVQWCDLGSLKSPPGSSDSPASASRVAGITGM 49
                                                                                                                                                                                                                                                                                        Score 144; DB 7; Length 100;
Pred. No. 4.2e-11;
7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                         1 FFFFFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #3277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 663; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU32786 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                             58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                      Query Match .
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                   Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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stimulation, as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cancer, ulcer, HIV infection, human immunodeficiency virus, antinflammatory; antirheumatic, antiarthritic; immunosuppressive; antiarterial, endocrine, cardiant, central nervous system; virucide; antiafereial, endocrine, cardiant, central nervous system; virucide; antiafergica, antimutagn, cardiovascular; antianaemic; anaemic; antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermacological; antiafergic, antiasthmatic; antidiabetic; ortostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic Shock; pancreatitis; cardiac disease; haematopoietic disorder; platelet disorder; asthma; hirmomocytopeneia; osteoprosais; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM5963. The proteins can have activities based on the tissues and of they are expressed in such as: antiinflummatory; antirheumatic; antiarthitic; immunosuperssive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiagraph; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
                                                                                                                                                 Gaps
                                                                                                                                                 ;
0
                                                                                                             Length 112;
                                                                                                                                               9; Indels
                                                                                                                                                                                  47
                                                                                                                                                                                                                      44
                                                                                                                                                                                                       4 FFLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITG
                                                                                                         Score 143; DB 4;
Pred. No. 6.4e-11;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:1054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 212; 1217pp; English.
                                                                                                                                                                                                                                                                                                                AAM25539 standard; protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C, Drmanac RT;
                                                                                                             57.78;
65.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000WO-US035017
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-457603/49.
                                                                                                                              Local Similarity
ses 29; Conserv
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                                                                            Sequence 112
                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                    AAM25539;
                                                                                                               Query Match
                                                                                                                                    Best Loca
Matches
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antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthitis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoprosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple solerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the
                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                                                                                                                                                                                                                                                                                                                                                                                     FFFLRWSFALVAQAGVQWHDLGSLQPPAPGFKRFSSLSLLSRWDYRHAHARLIFVFLVEM 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                 Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vaccination; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                               Score 140.5; DB 4;
Pred. No. 2.6e-10;
l; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --SSDSRASASQSARITGV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GFLHVGQAGLELPTŚGDPPTSAŚQSARITGV 99
                                                                                                                                                                                                                                                                                                                                                                                              3 FFFLRQSFIL-SQAGVAWHDLGSLHPPLPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 281; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU30350 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted protein #841.
                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                 56.7%;
39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2001; 2001WO-US008656
                                                                                                                                                                                                                                                                                                                                                         36; Conservative
                                                                                                                                                                                                                                       neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 -----
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                              Sequence 194 AA;
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nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoissis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation, as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to bytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymorleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, mematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or resamment of canner, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                                                                                                                                                                                                                                                 FFFFFL-----RQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
                                                                                                                                                                                                                                                                                                                                                                          13 FFFFFLFFFETESCPVAQAGTQWCDLGSLQPPPPGXSNSPASASRVAGITGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 25672; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                               4; Length 110;
                                                                                                                                                                                                                                                             Score 138.5; DB 4
Pred. No. 2.5e-10;
5; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 25672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO11780 standard; protein; 52
                                                                                                                                                                                                                                                               55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating e.g. leukemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                         31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                       Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA011780;
                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
               889999999888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                            human, GPCR, guanosine triphosphate-binding protein coupled receptor, gene therapy.
                                                                  ij
                                 DB 4; Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 55.2%; Score 137; DB 7; Length 151; Best Local Similarity 61.1%; Pred. No. 5.6e-10; Matches 33; Conservative 4; Mismatches 11; Indels
                               55.4%; Score 137.5; DB 4; Length ilarity 68.2%; Pred. No. 1.4e-10; Conservative 1; Mismatches 12; Indels
                                                                                                                       4 FFFFFRMSFVLVAQAGVQMHDLGSPQPPPPGFKHSPASASQVA 47
                                                                                                   1 FFFFFLRQSFTL-SQAGVAWHDLGSLHPPLPGSSDSRASASQSA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suwa M, Asai K, Akiyama Y, Aburatani H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 1382; 28pp; English.
                                                                                                                                                                                                                        ADC86929 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                               Human GPCR protein SEQ ID NO:1382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002; 2002EP-00013517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-2001; 2001JP-00246789.
                                                                                                                                                                                                                                                                                            (first entry)
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N-PSDB; ADC86928.
                               Query Match
Best Local Similarity
Matches 30; Conserv
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Sequence 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                            01-JAN-2004
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                                                                                                                                                                                                                                                           ADC86929;
                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                         ADC86929
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Search completed: August 10, 2004, 19:14:04 Job time : 55 secs

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RESULT 2
8-10-017-161-1912
; Sequence 1912, Application US/10017161
; Publication No. US20030143668A1
110
110
109.5
109.5
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112.5
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Sequence 1912, Ap
Sequence 1956, Ap
Sequence 1956, Ap
Sequence 1054, Ap
Sequence 1054, Ap
Sequence 1322, App
Sequence 1322, Ap
Sequence 132, Ap
Sequence 112, App
Sequence 112, App
Sequence 112, App
Sequence 112, App
Sequence 112, App
Sequence 112, App
                                                                                    August 10, 2004, 19:15:22 ; Search time 46 Seconds (without alignments) 327.321 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                     US-10-082-830-224
248
1 FFFFELRQSFTLSQAGVAWH......LPGSSDSRASASGSARITGV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-017-161-1912

US-10-292-798-1568

US-10-292-798-1604

US-10-198-070-82

US-10-198-070-82

US-10-108-260A-4804

US-10-108-260A-4804

US-10-108-260A-4804

US-10-108-260A-4804

US-10-108-260A-4804

US-10-108-20A-4804

US-10-108-070-112

US-10-198-070-112

US-10-198-070-112

US-10-198-070-112

US-10-198-070-112

US-10-198-070-112
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Maximum Match 100%
Listing first 45 summaries
                                                              - protein search, using sw model
                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Query
Match Length D
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153
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                                                                                                                                        Title:
Perfect score:
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Maximum DB
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12411
15411
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Sequence 58, Appl
Sequence 674, App
Sequence 304, Appl
Sequence 30, Appl
Sequence 1734, Appl
Sequence 1734, Appl
Sequence 1959, Appl
Sequence 1950, Appl
Sequence 1950, Appl
Sequence 1950, Appl
Sequence 1950, Appl
Sequence 1950, Appl
Sequence 1960, Appl
Sequence 1960, Appl
Sequence 1960, Appl
Sequence 2008, Appl
Sequence 2008, Appl
Sequence 2088, Appl
Sequence 2088, Appl
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Sequence 2088, Appl
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Sequence 2884, Appl
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100.0%; Score 248; DB 14; Length 48;
Best Local Similarity 100.0%; Pred. No. 6.1e-24;
Matches 48; Conservative 0; Mismatches 0; Indels
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-830-224
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RESULT 3

US-10-292-798-1568

JUS-10-292-798-1568

JUS-10-292-798-1568

JUSCOBORD NO. USZO030235833A1

JUSCOBORD NO. USZO03023583A1

JUSCOBORD NO. USZO03023583A1

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JUSCOBORD NAMBER: US/10/292,798

JUSCOBORD NAMBER: US/10/21,161

JUSCOBORD NAMBER: US/10/1,161

JUSCOBORD NAMBER: US/10/1,161

JUSCOBORD NAMBER: US/10/1,161

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JUSCOBORD NAMBER: US/10/1,161

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JUSCOBORD NAMBER: US/10/1,161

JUSCOBORD NAMBER: US/10/1,
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61.7%; Score 153; DB 15; Length 176;
Best Local Similarity 66.0%; Pred. No. 2.7e-11;
Matches 31; Conservative 4; Mismatches 12; Indels (
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GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: SUWA, MAKIKO
APPLICANT: ARIXAN, KIYORIA
APPLICANT: ARYZWA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT PELING DATE: 2002-12-18
FRICH RAPLICATION NUMBER: US/10/017,161
CURRENT PELING DATE: 2002-06-18
FRICH RAPLICATION NUMBER: US/10/246789
FRICH RAPLICATION NUMBER: US/201/246789
FRICH RAPLICATION NUMBER: 2021-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1912
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Best Local Similarity 66.0°
Matches 31, Conservative
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; ORGANISM: Homo sapiens
US-10-017-161-1912
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; ORGANISM: Homo
US-10-292-798-1568
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| JERUKALL INFORMATION:
| JERUKAL INFORMATION:
| APPLICANT: ASAI, KIYOSHI
| APPLICANT: ASAI, KIYOSHI
| APPLICANT: ASAI, KIYOSHI
| APPLICANT: ASAI, KIYOSHI
| APPLICANT: ASAI, KIYOSHI
| APPLICANT: AUGUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
| FILE REPERBENCE: 084335/166
| CURRENT APPLICATION NUMBER: 10/017,161
| PRIOR FILING DATE: 2001-12-18
| PRIOR FILING DATE: 2001-12-18
| PRIOR FILING DATE: 2001-06-18
| PRIOR FILING DATE: 2001-06-18
| NUMBER OF SEQ ID NOS: 2070
| SOFTWARE: PALENTIN VEF: 2.1
| SEQ ID NO 1604
| LENGTH: 217
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Sequence 82, Application US/10198070

Publication No. 220030109437A1

GENDEAL INFORMATION:
APPLICANT: AVERBACK, PAUL

APPLICANT: GENERAL, WERTHELL, WERTHELL, WERTHELL INFORMATION:
TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

FILE REFERENCE: 59003.000008

CURRENT APPLICATION NUMBER: US/10/198,070

CURRENT PILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,161

PRIOR APPLICATION NUMBER: 60/306,161

PRIOR PAPLICATION NUMBER: 60/306,150

PRIOR FILING DATE: 2001-07-19

PRIOR PLING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,150

PRIOR APPLICATION NUMBER: 60/331,477
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                                                                                                                                                                                                                                                                                                                      Length 217;
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CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILLING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1604, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 68.1
Matches 32; Conservative
                                                                                                                                                                                                            TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1956
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CORGANISM: Homo sapiens
US-10-292-798-1604
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Query Match
Best Local Similarity
Matches 33; Conserv
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US-10-292-798-1382
                                                                                                            RESULT 9
US-10-017-161-1726
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Publication No. US20040053248A1

GENERAL INFORMATION:

APPLICANT: Hyeeq Inc

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/296,115

CURRENT APPLICATION NUMBER: US/948,725

PRIOR REPLICATION NUMBER: US09/488,725

PRIOR PAPLICATION NUMBER: US09/488,725

PRIOR APPLICATION NUMBER: US09/552,317

NUMBER OF SEQ ID NOS: 1478

LENGTH: 194
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Publication No. US20040005560A1

GENERAL INFORMATION:

APPLICANT: HELIX ESERACH INSTITUTE

TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA

FILE REPRESENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4804
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Best Local Similarity 62.5%; Pred. No. 2e-10;
Matches 30; Conservative 7; Mismatches 11; Indels (
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PRIOR FILING DATE: 2001-11-16
                 NUMBER OF SEQ ID NOS: 125
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 82
LENGTH: 100
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US-10-108-260A-4804
                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-198-070-82
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US-10-296-115-1054
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Publication No. US2003023833A1

Publication No. US2003023833A1

GENERAL INFORMATION:

APPLICANT: SUMA, MAKIXO

APPLICANT: ARIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI

APPLICANT: ABURATANI, HIROYUKI

TILLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REPRENCO: 084335/166

CURRENT APPLICATION NUMBER: US/10/292,798

CURRENT PILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: 10/017,151

PRIOR APPLICATION NUMBER: 10/017,151

PRIOR APPLICATION NUMBER: 10/017,151

PRIOR APPLICATION NUMBER: 10/017,151

PRIOR APPLICATION NUMBER: 10/017,161

PRIOR APPLICATION NUMBER: 10/010-246789
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                               55.2%; Score 137; DB 14; Length 151; 61.1%; Pred. No. 2.4e-09; cive 4; Mismatches 11; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
1 FFFFTLRQSFTLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARITGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                     APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, HIROYUKI
ITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152 us/10/017,161
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1726
LENGTH: 151
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Pred. No. 2.4e-09;
4; Mismatches 11;
                                                                                                                                                                                    Sequence 1726, Application US/10017161; Publication No. US20030143668A1; GENERAL INFORMATION:
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Best Local Similarity 61.1%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2..
SEQ ID NO 1382
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US-10-292-798-1382
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US-10-017-161-1726
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APPLICANT: AVENALA, TACK
TITLE OF INVENTION: CEDIMELL, JACK
TITLE OF INVENTION: CEDIMELL, CADIMING THE TREATMENT OF TUMORS AND OTHER
TITLE OF INVENTION: CEDIME
TITLE OF INVENTION: CEDIME
TITLE OF INVENTION: CEDIME
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TITLE OF INVENTION: CEDIME
TITLE OF INVENTION: CEDIME
CURRENT APPLICATION NUMBER: US/10/198,070
CURRENT PILING DATE: 2002-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR PELING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2011-11-16
NUMBER OF SEQ ID NOS: 125
SOOTWARE: PATENTIN VET: 2.1
SEQ ID NO 112
THENGEN: NUMBER: DATE: 2011-11-16
SEQ ID NO 112
THENGEN: NUMBER: DATE: 2011-11-16
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THENGEN: DATE: 2011-11-1
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US-10-104-047-2674

; Sequence 2674, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESERCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REPERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT PILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PARENTIN Ver. 2.1
; SEQ ID NO 2674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.6%; Score 133; DB 15; Length 1 Best Local Similarity 54.2%; Pred. No. 7.2e-09; Matches 26; Conservative 7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FFFFLRQSFTL-SQAGVAWHDLGSLHPPLPG-----
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, Publication No. US20030077808A1
, GENERAL INFORMATION:
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Best Local Similarity 38.0
Matches 35, Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-2674
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US-10-198-070-112
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US-09-764-891-4323
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                                                                                                                                                                                                                                                   TYPE: PRT
TYPE: PRT
TYPE: PRT
PROGRAMISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
OCHER NIPORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (48)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOCATION: (53)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-4323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 126; DB 14; Dred. No. 9e-08; Indels
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US-10-017-161-1698

// Sequence 1689, Application US/10017161

// Publication No. US20030143668A1

// Publication No. US20030143668A1

// GENERAL INFORMATION:

// APPLICANT: SUMA, MAKIKO

// APPLICANT: AALTYAMA, YUTAKA

// APPLICANT: AALTYAMA, YUTAKA

// APPLICANT: ABURATANI, HROYUKI

// TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

// TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED

// TURRENT APPLICATION NUMBER: US/10/017,161

// CURRENT APPLICATION NUMBER: US/2001/246789

// PRIOR PILING DATE: 2001-06-18

// SEQ ID NOS: 2430

// SEQ ID NO 1698

// LENGTH: 220

// LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.4%; Score 130; DB 10;
Best Local Similarity 71.4%; Pred. No. 6.4e-09;
Matches 25; Conservative 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SVTQAGVQWHNLGSLQPPLPGSSDSPASASQVAGV 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 TLSQAGVAWHDLGSLHPPLPGSSDSRASASQSARI 45
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; Publication No. US20030235833A1
; GENERAL INFORMATION:
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-292-798-1354
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| APPLICANT: ABURATANI, HIROYUKI
| TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
| TITLE PEPERBRUE: 084335/166
| CURRENT APPLICATION NUMBER: US/10/292,738
| CURRENT FILING DATE: 2002-11-13
| PRIOR PILING DATE: 2000-12-18
| PRIOR PILING DATE: 2001-12-18
| PRIOR PILING DATE: 2001-06-18
| PRIOR PILING DATE: 2010-06-18
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